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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein September 21, 2001, 16:51:56; Search time 22.23 Seconds Run on:

(without alignments) 1475.375 Million cell updates/sec

Title: Perfect :

US-09-236-468A-2 2907 1 MAWLGASLHVWGWLMLGSCL......DDILMEKPSRPMESNPDTEG score:

541

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

412676 segs, 60623988 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SID8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SID8/gcgdata/geneseqg/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

SUMMARIES

Description	G-protein parathyr	Human PTR2 seven t	Human PTH2 recepto	Rat PTH2 receptor	Zebrafish parathyr	Zebrafish PTH1R re	Opossum kidney PTH	Parathyroid hormon	Opossum kidney PTH	Opossum kidney PTH	Parathyroid hormon
ΩI	AAW12695	AAB71875	AAB80560	AAB80559	AAY99600	AAY90230	AAR92276	AAW73315	AAR27705	AAR92275	AAW73314
DB	18	22	22	22	21	21	17	20	13	17	20
% Query Match Length DB ID	541	550	550	546	536	536	585	585	585	515	515
% Query Match	100.0	90.6	90.3	76.3	48.8	48.8	47.9	47.9	47.9	47.7	47.7
Score	2907	2635	2626	2217.5	1418.5	1418.5	1392	1392	1391	1388	1388
Result No.	1	7	٣	4	2	9	7	80	6	10	11

ALIGNMENTS

G-protein parathyroid hormone receptor; HLTDG74; parathormone; PTH: calcium; signal transduction; agonist; antagonist; hypocalcaemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephroliasis; therapy; diagnosis. G-protein parathyroid hormone receptor HLTDG74. 541 AA AAW12695 standard; Protein; 95WO-US07085 (first entry) Homo sapiens WO9639433-A1 05-JUN-1995; 12-DEC-1996. 31-MAY-1997 AAW12695; RESULT

95WO-US07085. 05-JUN-1995; (HUMA-) HUMAN GENOME SCI INC

Soppet DR;

Ruben SM,

Rosen CA,

Li Y,

WPI; 1997-043068/04.

N-PSDB; AAT59619

Human G-protein parathyroid hormone receptor, HLTDG74 - used to

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PTR2 seven transmembrane domain.

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                                            A novel 7-transmembrane receptor (AAW12695) has been identified as a human G-protein parathyroid hormone (PTH) receptor, designated HLTDG74. It shows 48.2% homology to the human PTH receptor. Its amino acid sequence was deduced from a conva clone (AAT59619) isolated from a human T cell lymphoma tissue cDNA clone (AAT59619) isolated HLTDG74 can be produced in transformed host cells and used to screen for (ant)agonist cpds. Agonists may be used to prevent treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism and chronic tetany by stimulating an increase in serum calcium levels. Antagonists can be used to inhibit the receptor e.g. for the treatment of osteoporosis, hyperchlosenia, hypoparathyroidism, hypertatment.
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hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
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                              English.
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Matches 541; Conservative
                            9; Fig 1A-E; 62pp;
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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h15571. h15571 GPCR polymclectides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory diseases including asthma, allergies (e.g. allergic thinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, graft versus host disease, cystic fibrosis and, in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR mithodies may be used as diagnostic agents for detecting the presence of GPCR may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory; vascular; hepatic; antiasthma; anitmicrobial; antiinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoimmunity; graft rejection; cystic fibrosis.
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6; Mismatches
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Best Local Similarity 91.4
Matches 500; Conservative
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parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic; parathyroid hormone receptor; anorectic; nootropic; antimigratine; antidiabetic; osteopathic; hypertensive; cardiant; cytostatic; antidiabetic; neuroprotective; PTH receptor antigonist; obesity; eating disorder; metabolic disorder; mental disorder; headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism; hypertension; congestive heat failure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis;
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                                                                                                                          VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT 300
                                                                                                                                                                                                     LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEV 420
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                                                                                                                                                                                                                                                                                                                                     other
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                          New parathyroid hormone type 2 or 1 receptor ligand, useful for treating e.g. migraine or headaches, hypertension, obesity and ot eating or metabolic disorders, mental disorders and osteoporosis
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activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 tor PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyellnating conditions such as multiple sclerosis and leukodystrophies. The present sequence represents a PTH2 receptor which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 cytostatic, antiasthmatic and neuroprotective
                                                                                                                                                                                                                                                                                                                                                          61 GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
                                                                                                                                                                                                                                                                                                                                                                         121 NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIH 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAWLGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE
                                                                                                                                                                                                                                                                                                                  LPRSPADSLTATSLYLAMSGVTQSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 lakstlvlvlvfgvhyivfvclphsftglgweirmhcelffnsfggffvsilycycngev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAAAHAWCL---SLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                         Length 550;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                        Score 2626; DB 22;
Pred. No. 2.2e-276;
6; Mismatches 30;
                                                                                                                                                                     exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat PTH2 receptor amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB80559 standard; Protein; 546 AA
                                                                                                                                                                                                                                        90.3%;
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                                                                                                                                                                                                                                                                     499; Conservative
cardiant,
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                 550 AA;
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 hypertensive,
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                                                                                                                                                                                                   Sequence
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Best Local S
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AAB80559
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The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (ID) or PTH1 receptor ligand (ID). (I) has anorectic, neuroleptic, antidepression, nootropic, analgesic, antimigratine, antidabetic, osteopathic, hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective activities, and is an PTH receptor antiasthmatic and neuroprotective activities, and is an PTH receptor antiagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or hypercalcaema and other metabolic disorders, osteoporosis, hypercalcaema and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. The present sequence represents a PTH2 receptor which is used in the
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                               PTH2 receptor binding activity; antidepression; neuroleptic; analgesic; antinigraine; antidabetic; osteopathic; hypertensive; cardiant; cytostatic; antidabetic; neuroprotective; PTH receptor antagonist; obesity; eating disorder; metabolic disorder; mental disorder; depression; schizophrenia; dementia; acute pain; chronic pain; migraine; hypertension; congestive hart fallure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis;
parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New parathyroid hormone type 2 or 1 receptor ligand, useful for treating e.g. migraine or headaches, hypertension, obesity and other eating or metabolic disorders, mental disorders and osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAWLGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 60
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76.7%; Pred. No. 5.7e-232;
.1ve 37; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig I; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                              15-JUN-2000; 2000WO-US16776
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139335
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Matches 417; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 AA;
                                                                                                                                                                                                   Leukodystrophy.
                                                                                                                                                                                                                                                                              WO200077042-A2.
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(PTHIR) from the zebrafish. Its coding seequence was obtained by sequencing a cDNA clone. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zebrafish; parathyroid hormone type-1 receptor; PTH1R; developmental disorder; physiological disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding parathyroid hormone receptors PTHIR and PTHIR, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence
QAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPR
                                                                                                                                                                                                                                   SPA---DSLTATSLYLAMSGVTQSRTASHTLSTRSNKEDSGRQRDDILMEKPSRPMESNP
                                                                                                                                                                                                                                                              478 tacrqidshvtlpgyvwssseqdcqpqs---tpeetkkghgrqeddspvgessrpvaft1
                                                         LADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK
                                                                                                                  LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is the parathyroid hormone type-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebrafish parathyroid hormone type-1 receptor PTH1R.
                                                                                                                                                                                                                                                                                                                                                                                            AAY99600 standard; Protein; 536 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jueppner H, Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio.
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                                                                                                                                                        240
                                                                                                                                                                                                     300
                                                                                                 GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
                                                                                                            NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIH 180
                               Gaps
                                                                          9
                                                     4 LGASLHV--WGWLMLGSCL-LARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 60
                                                                                                                                                                                                                                                                                                                                          MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
                                                                                                                                                                                                                                     241 VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT
                                                                                                                                                                                                                                                                                  LADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK
                                                                                                                                                                                                                                                                                                                               LAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGE
                              6
                Pred. No. 4e-145;
Pred. No. 4e-145;
Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                          420 VQAEVKKMWSRWNLSVDWKRTPPCGSR--RCGSVL--TTVTHSTS 460
                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
48.8%; Scc. No. 4C
57.8%; Pred. No. 4C
14.4 80; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zebrafish PTH1R receptor protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY90230 standard; Protein; 536
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                              269; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JUEP/) JUEPPNER H. (RUBI/) RUBIN D A.
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio.
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         Query Match
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                              Matches
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This sequence is a parathyroid hormone receptor type I (PTHIR)
receptor protein of the invention. The invention also relates to a PTH3R
receptor protein. Anagonists of PTHIR or PTH3R can be used for the
treatment of diseases associated with an increase in PTHIR or PTH3R
activity, respectively. The peptides are used for diagnosis or prognosis
of diseases and disorders associated with PTHIR or PTHIR, such as cancer.
The polypeptides can be used as a molecular weight markers on sodium
dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
on molecular sieve gel filtration columns. Antigenic epitope-bearing
peptides and polypeptides are useful to raise antibodies, including
monoclonal antibodies, that bind specifically to a polypeptide. The
peptides are useful during diagnosis of diseases and disorders in
mammals involving PTHIR or PTH3R receptor expression or function.
Mutations that affect PTHIR or PTH3R sequence and/or expression levels
of PTHIR or PTH3R could be diagnostic for patients with disease or
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                                                                                                                                                                                                                                                                                                                                                           disorders of a developmental, physiological or neurological nature, nucleic acid molecules are valuable for chromosome identification. T mapping of DNAs to chromosomes is an important first step in correlating those sequences with genes associated with disease.
receptor 1 for treating disorders associated with receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LGASLHV:-WGWLMLGSCL-LARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILLIGWGFPAAFVAAWAVARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%; Score 1418.5; DB 21; Lengt
57.8%; Pred. No. 4e-145;
.ive 80; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 VQAEVKKMWSRWNLSVDWKRTPPCGSR--RCGSVL--TTVTHSTS 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR92276 standard; Protein; 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                    2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1996
                                                  Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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Abou-Samra A,
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06-JUN-1995;
                                                                                                                                                                                                                                                                      08-FEB-1999
                                                                                                                                                                                                                                                                                                                  Parathyroid
                                                                                                                                                                                                                                                                                                                             PTH-related
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                                                                                                                                                                                                                                               AAW73315;
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                                381
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                                                                                                                                                                                                                                                                                                                                              Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) receptors (AAR92275 and AAR92775) are encoded by CDNA clones OK-H (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2 separate genes or of a laboratory artifact. The receptor induces an increase in intracellular cAMP and calcium when challenged with PTH or PTHrP. Recombinant receptors can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hyporaclacemia, to screen for (ant)agonists and to raise antibodies. Host cells expressing the receptor can be used for diagnostic measurement of PTH serum levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|:| || |||||:||: |: || || 24 alvdaddvitkeeqiillrnaqaqceqrlkevlrvpelaesakdwmsrsaktkkekpaek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFIL
                    Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer; opossum.
                                                                                                                                                                                                                                                                                DNA encoding vertebrate parathyroid hormone receptor - useful diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                               Potts JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.9%; Score 1392; DB 17;
Best Local Similarity 47.8%; Pred. No. 3.5e-142;
Matches 274; Conservative 92; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE-
                                                                                                                                                                                                               Kronenberg HM,
Opossum kidney PTH/PTHrP receptor,
                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 2A-2E; 64pp; English.
                                                                                                                                 91US-0681702
                                                                                                                                                      92US-0864475
91US-0681702
                                                                                                                                                                                                            Abou-Samra A, Juppner H,
Schipani E, Segre GV;
                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
                                                                 Didelphis virginiana
                                                                                                                                                                                                                                              WPI; 1996-139028/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 AA;
                                                                                                                                                                                                                                                          N-PSDB; AAT15946
                                                                                                                                 05-APR-1991;
                                                                                                                                                                   05-APR-1991;
                                                                                                                                                       06-APR-1992;
                                                                                     US5494806-A
                                                                                                           27-FEB-1996
                                                                                                                                                                                                                                                                                                      cancer etc.
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                    494 vshtsvtnvgprgglalsls--prlapgagasanghhqlpgyvkhgsisen-slpssgpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF
                                                                                   FNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPQGSRRCGSVLTTVTH---
                                                                                                                                                                           -STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor; PTH receptor; antibody; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody to parathyroid hormone receptor - for diagnostic or therapeutic use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1392; DB 20;
Pred. No. 3.5e-142;
2; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE-
                                                                                                                                                                                                                                                                 539
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                                                                                                                                                                                                                                                                 SGRQRDDILM------EKPSRPMESNPDT
                                                                                                                                                                                                                                                                                                           551 pgtkddgylngsglyepmvgeqppplleeeret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypercalcaemia; opossum.
                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parathyroid hormone receptor OK-O.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW73315 standard; Protein; 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
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91US-0681702.
95US-0471494.
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47.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormone
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N-PSDB; AAV08389.
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Best Local Similarity
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TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400
                                                                                                                                                                                                                                                101
                                               341
                                                                                                                                                                                                                                      FNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTH--- 457
 GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFR
                                     HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV
                                                                                                                                                         IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA
                                                                                                                                                                                                                                                                              -STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED
                                                                                                                   SIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis and treatment of tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parathyroid hormone; related protein; calcium; antagonist; antibodies; hypercalcaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                     517 SGRORDDILM-----EKPSRPMESNPDT 539
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                                                                                                                                                                                                                                                                                                                                       pgtkddgylngsglyepmvgeqppplleeeret
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1991;
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Disclosure; Fig 2; 91pp; English.
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The parathyroid hormone/parathyroid hormone related protein (PTH/PTHFP)

receptor protein sequence was deduced form the DNA sequence of the
clone OK-0, isolated from opossum kidney (OK) cells. The clone OK-0
is identical to the OK-H clone exept at the C-terminal tail as OK-0
is identical to the OK-H clone exept at the C-terminal tail as OK-0
clonedes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
The difference is attributed to a single nucleotide deleted in the OK-H
companies of the companies of the opening opening opening of the opening opening opening of the opening openi

585 AA; Sequence

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                                                                                                                                                                                                                                                                                                                                                           282 IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA 341
                                                                                                                                                                                                                                                                                                                                                                                        380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED 516
                                                                                                                                                                              102 HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV 161
                                                                                                                                                                                                                                        162 AILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQN 221
                                                                                                                                                                                                                                                                                                   222 SIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFIL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNSFQGFFVSIIYCYCNGEVQAEVKKMMSRWNLSVDWKRTPPCGSRRCGSVLTTVTH--- 457
                                                           24 AQLDSDGTITIEEQIVLVLKAKVQCELNIT------53
                                                                                                                                     | :|:| || || ||||:| |: || || :
24 alvdaddvitkeeqiillrnaqaqceqr1kevirvpelaesakdwmsrsaktkkekpaek
                                                                                                                       --AQLQEG-----EGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFR
                                                                                                                                                                                                                                                                                                                                                                           10;
Length 585;
47.9%; Score 1391; DB 13; Length 947.8%; Pred. No. 4.5e-142; Live 93; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGRQRDDILM------EKPSRPMESNPDT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 pgtkddgylngsglyepmvgeqppplleeeret 583
                                Conservative
Query Match
Best Local Similarity
                                Matches 274;
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AAR92275 standard; Protein; 515 AA

RESULT 10

AAR92275

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therapeutic
                                                                                                                                                                                                                                                                                                                                                                05-APR-1991;
06-JUN-1995;
                                                                                                                                                                                                    08-FEB-1999
                                                                                                                                                                                                                                            Parathyroid
                                                                                                                                                                                                                                                     PTH-related
                                                                                                                                                                                                                                                                                            US5840853-A
                                                                                                                                                                                                                                                                                                              24-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                          Schipani E,
                                                                                                                                                                                                                                                                                                                                                                                                                 Abou-Samra
                                                                                                                                                                                 AAW73314;
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                                                                                                                                                                                                                                                                                                                                                  Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) receptors (AAR92375 and AAR92776) are encoded by CDNA clones OK-H (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2 separate genes or of a laboratory artifact. The receptor induces an increase in intracellular cAMP and calcium when challenged with PTH or PTHrP. Recombinant receptors can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocaloaemia, to screen for (ant)agonists and to raise antibodies. Host cells expressing the receptor can be used for diagnostic measurement of PTH serum levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFIL 281
                                                                                                                                                                                                                                                                                            useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer; opossum.
                                                                                                                                                                                                                                                                                            e.g. hypercalcaemia, hypo-calcaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                          ing vertebrate parathyroid hormone receptor and treatment of e.g. hypercalcaemia, hypo-
                                                                                                                                                                                                                                 Potts JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%; Score 1388; DB 17;
54.6%; Pred. No. 7.9e-142;
11ve 73; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE----
                                                                                                                                                                                                                                 Kronenberg HM,
                                     Opossum kidney PTH/PTHrP receptor.
                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-1E; 64pp; English
                                                                                                                                                                               92US-0864475
91US-0681702
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                  (first entry)
                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP
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                                                                                                                                                                                                                                , Juppner I
Segre GV;
                                                                                                 Didelphis virginiana
                                                                                                                                                                                                                                                             WPI; 1996-139028/14.
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                                                                                                                                                                                                                                                                      N-PSDB; AAT15945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515
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                                                                                                                                                                                                                                                                                            encoding
                                                                                                                                                           05-APR-1991;
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                  18-MAY-1996
                                                                                                                   US5494806-A
                                                                                                                                       27-FEB-1996
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Matches 254;
                                                                                                                                                                                                                                          Schipani E,
                                                                                                                                                                                                                                                                                                              cancer etc.
AAR92275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 lypqaeesrevsdrsrlqdgfclpewdnivcwpagypgkvvavpcpdyfydfnhkgrayr 143
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                       IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA
                                                                                     TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; PTH receptor; antibody; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.7%; Score 1388; DB 20; 54.6%; Pred. No. 7.9e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypercalcaemia; opossum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parathyroid hormone receptor OK-H.
                                                                                                                                                                                                                                                                                                                                   AAW73314 standard; Protein; 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0864475.
91US-0681702.
95US-0471494.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAV08388.
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parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
                                                                       321 fgwglpavfvavwvtvratlantecwdlssgnkkwilqvpilaaivvnfilfiniirvla 380
                                                                                                                                                                                                                                                 AILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQN 221
 HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor protein sequence was deduced form the DNA sequence of the clone OK-H, isolated from opossum kidney (OK) cells. The protein may be used in a therapeutic compsn. to inhibit activation of PTH or PTH.P and thus reduce the level of calcium in the blood. Cpds. capable of competing with PTH or PTH.P for binding can be identified using the protein prod. and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The protein may be used for the prodn. of antibodies useful for the treatment,
                                                                                                                222 SIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFIL
                                                                                                                                                                         282 IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA
                                                                                                                                                                                                                                 342 TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding parathyroid hormone receptor, DNA and antibodies or (differential) diagnosis of hypercalcaemia, and diagnosis treatment of tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parathyroid hormone; related protein; calcium; antagonist; antibodies; hypercalcaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Opossum kidney PTH/PTHrP receptor prepd. from clone OK-H.
                                                                                                                                                                                                                                                                                         401 FNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGS 445
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                                                                                                                                                                                                                                                                                                                                                                                            AAR27704 standard; Protein; 515 AA
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92US-0864475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypercalcaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Didelphis virginiana
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06-APR-1992;
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   S
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                                                                                                                                                                                                                                                                                          160 AVAILIIGYFREHCTRNYIHMHLFVSFMERATSIFVKDRVVHAHIGVKELESLIMQDDP
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                                                                                                                                                                                         ----TAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVA
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                                                                                                                                                                                                                                                                                                                                                                                            ILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRV
classification, prognosis and/or treatment of disorders related
the interaction between a cell receptor and a ligand such as in
hypercalcaemia. See also AAR27705-16.
                                                                                                                50;
                                                                                       Length 515;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AQLDSDGTITIEEQIVLVLKAKVQCELNI-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 LFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGS
                                                                                       DB 13;
                                                                                                                88;
                                                                                                    2e-140;
                                                                                                               76; Mismatches
                                                                                      47.3%; Score 1375; 54.2%; Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PTRR seven transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB71876 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000; 2000WO-US21278
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                                                                                                                Conservative
                                                    AA;
                                                                                                    Similarity
 classification,
                                                  515
                           hypercalcaemia.
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                                                                                                    Best Local Sim:
Matches 253;
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                                                    Sequence
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                                                                                       Query Match
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546 etlettppamaapkddgflngscsgldeeasgperppallge 587

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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR of comparison with the seven transmembrane domain of a novel GPCR designated h15571. h15571 GPCR polymorleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory diseases including asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graff rejection, graff versus host disease, organ-specific autoimmunity, particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies and antagonists) of GPCR expression and activity. The anti-GPCR antibodies and decreating the presence of GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                        leic acids encoding a G-prot. coupled receptor polypeptides, useful
preventing, diagnosing and treating, e.g. liver fibrosis and asthma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1336.5;
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                                                                                                                                Disclosure; Fig 2; 145pp; English.
               Weich NS
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Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             polypeptides in samples
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                                          WPI; 2001-138653/14
                                                                                                                                                                                                                                                                                                                                                                                                                           593 AA;
               Lloyd
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              Hodge MR,
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parathyroid hormone receptor - useful for of e.g. hypercalcaemia, hypo-calcaemia,
                                                                                                                                                                                                                         Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer.
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/label= Transmembrane_region
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                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                Ā
                                            AAR92277 standard; Protein; 591
                                                                                                                                                                                  Rat bone PTH/PTHrP receptor
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Schipani E, S
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RESULT 14
AAR92277
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Claim 1; Fig 3A-3E; 64pp; English.

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                                                                                                                                                                                                                                                                                                                                                    96
          A rat parathyroid hormone/parathyroid hormone-related protein (PTH/PTHP) receptor (AAR92277) is encoded by CDNA clone RISB (AAT15947) isolated from a rat osteosarcoma ROS 17/2.8 CDNA library. The receptor a G-protein linked receptor having 7 transmembrane domains. It induces an increase in increase in increase in can produced in vector and oalcium upon challenge with PTH or PTHPP. Recombinant receptor can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host cells expressing the receptor are used for diagnostic measurement of PTH
                                                                                                                                                                                                                                                                                                         GVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISF
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                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                                           Mismatches 136; Indels
                                                                                                                                                                                                                                                                                        22 ARAQLDSDGTITIEEQIVLVLKAKVQCE-----LNITAQLQEGEGN---
                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                Score 1331.5; DB 1
Pred. No. 1.4e-135;
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                                                                                                                                                                                                                                                                       Antibody to parathyroid hormone receptor - for diagnostic therapeutic use
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                                                                                                                                                                                              Potts JT;
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46.6%; Pred. No. 1.4e-135;
Live 86; Mismatches 136;
                                                                                                                                                                                              Kronenberg HM,
                                                                                                                                                                                                                                                                                                             English.
                                                                                                              92US-0864475.
91US-0681702.
95US-0471494.
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Matches 270; Conserv
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                                                                                     06-JUN-1995;
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             Rattus sp.
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Qy 502 RTASHTLSTRS-------NKEDSGRQRDDILMEK 528
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547 etlpvtmavpkddgflngscsgldeeasgsarpppllge 585

Search completed: September 21, 2001, 17:05:44 Job time: 828 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_68:*
1: pir1:*
2: pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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gastric inhibitory growth hormone-rel	glucagon receptor glucose-dependent growth hormone-rel	calcitonin recepto glucagon receptor	calcitonin recepto	calcitonin recepto	calcitonin recepto growth hormone-rel	calcitonin recepto	CAICILONIN recepto CRF receptor - mou
153273 146586	JU1957 137411 S29753	137217 JC4363	149154 533746	S34486 A37430	160800 S29754	A39285	14/130 149149
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growth hormone_rel glucagon receptor glucose_dependent growth hormone_rel calcitconin receptor calcitconin receptor calcitconin recepto	RESULT 1 A57519 parathyroid hormone receptor 2 precursor - human N;Alternate names: PTH2 receptor C;Species: Homo sapiens (man) C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Species: Homo sapiens C;Species: A;Species: A;Sp	tch 30.6%; Score 2635; DB 2; Length 550; 31 Similarity 31.4%; Pred. No. 8.6e-214; 32.60; Conservative 41 Mismatches 42 Indels 43; Todels 43; Todels 43; Todels 43; Todels 43; Todels 43; Todels 44; Todels 45; Todels 46; Mismatches 47; Todels 47; Todels 48; Todels 48; Pred. No. 8.6e-214; 48; Todels 48; Pred. No. 8.6e-214; 48; Todels 48; Todels
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A; Status: preliminary
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A; Molecule type: mRNA
A; Residues: 1-593 <CGN-
A; Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A; Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A; Title: Cloning and functional expression of a human parathyroid hormone receptor.
A; Reference number: 138113; MUID:93387403
A; Title: Cloning and functional expression of a human parathyroid hormone receptor.
A; Reference number: 138113; MUID:93387403
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-593 <- REL>
A; Residues: 1-593 <- REL>
A; Residues: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
R; Evvine, M.
Submitted to the EMBL Data Library, November 1994
A; Reference number: G07787
                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sopiens (man)
K; Schipani, E.; Weinstein, L.S; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhrmann, Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
X; Tille: Eseudohypoparathyroidism type ID is not caused by mutations in the coding ex A; Reference number: 138139; MUID:95263723
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A; Cross-references: EMBL:U22409; NID:g897594; PIDN:AAB60657.1; PID:g897596
A; Cross-references: EMBL:U22409; NID:g897594; PIDN:AAB60657.1; PID:g897596
B; Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, Endocrinology 132, 2157-2165, 1993
A; Title: identical complementary deoxyribonucleic acids encode a human renal and bone A; Reference number: A49191; MUID:93238641
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                                                                                                                                                                                                                                                                                                                    parathyroid hormone/PTH-related peptide receptor - human
N;Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
   A; Cross-references: EMBL: U17418; NID: 9596129; PIDN: AAA56774.1; PID: 9596130
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                                                                                                   ---EKPSRPMESNPDT
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Status: translated from GB/EMBL/DDBJ
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Best Local Si
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R.Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K.Schiner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K.A.Cession: A3286
A.Tile: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel A; Reference number: A3286
A.Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mesidues: 1-585 < JUE>
A; Cross-references: GB:M74445
C; Superfamily: glucagon receptor
C; Keywords: G protein-coupled receptor; transmembrane protein
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47.9%; Score 1392; DB 2;
Best Local Similarity 47.8%; Pred. No. 3.4e-109;
Matches 274; Conservative 92; Mismatches 137;
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Gaps

81

Oy 157 GSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESL 213 Db 200 ASLTVAVLILAYFRRLHCTRNYIHMHLFVSFMLRAVSIFVKDRVLYSGATLDEAERLTEE 259 Oy 214IMQDDPQINSIEATSVDKSQYIGCKIAVVMFIYFLATNYYMILVEGLYLHNLIFVAF 269 Db 260 ELRAIAQAPPPATAAAGYAGCRVAVTFFLYFLATNYYMILVEGLYLHNLIFVAF 269 Oy 270 FSDTKYLMGFILIGWGFPAAFVAAMAVARATLADARCWELSAGDIKWIYQAPILAAIGLN 329 Db 315 FSEKKYLMGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN 374 Oy 370 FSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN 374 Oy 371 FILELNTVRVLATRIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVVVCLPHS-FTG 388 OY 575 FILELNIVKLATRIRETNAGGDTRQQYRKLLKSTLVLWPLFGVHYIVFWAATPYTEVSG 434 OY 389 LGWEIRMHCELFFNSFOGFFVSIIYCYCNGEVQAEIKKSWSRWILSVDWKRTPDCGSRRC 448 OY 449 G-SVLTTVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTGRRT-AS 505 I	
RESULT 4 154195 parathyroid hormone/parathyroid hormone related-peptide receptor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000 C;Accession: 154195; A45698 C;Accession: 154195; A45698 A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (and rat genomes. A;Reference number: 154195; MUID:94292182 A;Reference number: 154195; MUID:94292182 A;Reference number: 154195 A;Reference number: 154195 A;Reference number: 1591 cRES> A;Residues: 1-591 cRES> A;Totos references: GB:L19475; NID:9467316; PIDN:AAA68098.1; PID:9467317 A;Rabou-Samra, A.B.: Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1998 A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid nof both cAMP and inositol trisphosphates and increases intracellular free calcium. A;Reference number: A42698; MUID:92212903	rmone-related pept musculus (house m musculus (house m 44203 ; van Dijk, T.B.; he EMBL Data Libra Expression patter mber: S44203 iminary e: mRNA 591 <kar> nces: EMBL:X78936; glucagon receptor</kar>
A;Accession: A42698 A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-585,'G',587-591 <abo> A;Experimental source: ROS 17/2.8 osteosarcoma cells A;Note: sequence extracted from NCBI backbone (NCBIP:92187) C;Superfamily: glucagon receptor</abo>	Best Local Similarity 52.4%; Pred. No. 1.8e-103; Matches 250; Conservative 70; Mismatches 97; Indels 60; Gap 22 ARAQLDSDGTITIEEQIVLVIKAKVQCELNITAQLQEGEGN
Ouery Match Best Local Similarity 46.6%; Pred. No. 4.2e-104; Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11; Qy 22 ARAQLOSOCITITEEDIVIVLKARVQCEINITAQLOEGEGN	OY 03
ADDVFTKEEQIFLLHRAQAOC 	Qy 157 GSLAVAILIIGYFRRLHCTRNYIHMHLEVSFMLRATSIFVKDRVVHAHIGVKELESL 213 Db 200 ASLTVAVLILAYFRRLHCTRNYIHMHMELSFMLRAASIFVKDAVLYSGFTLDEAERLTEE 259 Qy 214IMQDDPQNSIEATSVDKSQYIGCKIAVVMETYFLATNYWILVEGLYLHNLIFVAF 269 Cy 1 1 1 1 1 1 1 1 1 1

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C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C.Accession: S16319
R.Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, EMBD J. 10, 1653-1641, 1991
A.Title: Molecular cloning and expression of a CDNA encoding the secretin recept. A; Reference number: S16319, MUID:91266890
A; Accession: S16319
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-449 clsh
A; Residues: 1-449 clsh
A; Cross-references: EMBL:X59132; NID:957228; PIDN:CAA41849.1; PID:957229
C; Superfamily: glucagon receptor
C; Keywords: G protein-coupled receptor; transmembrane protein
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ET-NHYKRLAKSTLLLIPLFGIHYIVFAFSPED----AMEVQLFFELALGSFQGLVVAVL 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LLIRLLLLTKAA----HTVGVPPRLCDVRRVLLEERAHCLQQLSKEKKGALGPETASGCE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 VGCKLVMIFFQYCIMANYAWLLVEGLYLHTLLAISFFSERKYLQAFVLLGWGSPAIFVAL
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493 -SYGPMVSHTSVTNVGPRAG----LSLPLSPR 519
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C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change ll-Jan-2000
C;Accession: I59297
R;McCuaig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A;Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyroif A;Reference number: I59297; MUID:94255468
A;Reference number: I59297, MUID:94255468
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1.589 <RES
A;Cross-references: GB:L34611; NID:9530149; PIDN:AAA40011.1; PID:9530151
C;Genetics:
A;Gene: PTHR
A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45
C;Superfamily: glucagon receptor
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                                                            FILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTG 388
                                                                                                                                                                                                       GVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISF 156
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                                                                                                                                                                                                                                                                                                                                          FSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN
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llarity 50.2%; Pred. No. 2.5e-101;
Conservative 73; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPR 480
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Best Local Similarity
Matches 257; Conserv
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#status predicted <MAT>
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A;Residues: 1-284,588-460 <SRE>
A;Cross-references: GB:L13288; NID:9292903; PIDN:AAA36805.1; PID:9292904
R;Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Pessard, C.; Nicole, P.; Laburthe,
                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                          58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234
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                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 IYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQP---DISIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 FIKDMALF-------NSGEIDHCSEAS-VGCKAAVVFFQYCVMANFFWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 VHYIVEVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWE-LSAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWI
                                                                                                                                                                                                                                       DB 2; Length 459;
                                                                                                                                                                                                                                                                                                                         36 EQIVLVLKAKVQCELNITAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCP-
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 S--VDW--KRTPPCGSRR---CG---SVLTTVT----HSTSSQSQVA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
F;31-459/Product: vasoactive intestinal polypeptide rece
F;146-168/Domain: transmembrane #status predicted <TM1>
F;176-195/Domain: transmembrane #status predicted <TM2>
F;218-241/Domain: transmembrane #status predicted <TM3>
F;256-277/Domain: transmembrane #status predicted <TM4>
F;295-318/Domain: transmembrane #status predicted <TM5>
F;344-363/Domain: transmembrane #status predicted <TM6>
F;346-395/Domain: transmembrane #status predicted <TM6>
F;366-9100,292/Binding site: carbohydrate (Asn) (covale
                                                                                                                                                                                                                                     26.6%; Score 772.5; DB 2; 36.8%; Pred. No. 3.3e-57; ive 78; Mismatches 134;
                                                                                                                                                                                                                                                           Best Local Similarity 36.8 Matches 172; Conservative
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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C;Superfanily: glucadon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene. Reference number: S56014; MUID:97104266
                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vasoactive intestinal peptide receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: JH0594; S56014
R;Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-1819, 1992
A;Title: Functional expression and tissue distribution of a novel receptor for A;Reference number: JH0594; MUID:92232309
                                                                                                                                                                                                                                                                                                                                                                 71 ICWPRGTVGKISAVPCPPYIYDF-NHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPDISIG------KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 TLADARCWELSA-GDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 RKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNG 418
    A;Cross-references: EMBL:U20178; NID:g662795; PIDN:AAC50106.1; PID:g662796
                                                                                                                                                                                                                                                                                                                                                                                                         SCWPSSVPGRMVEVECPRFLRMLTSRNGSLFRNCTQDG------WSE-----TFP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 VVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                             13 WIMIGSCL--LARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNCFPEWDGL 70
                                                                                                                                                                                                                                                                                                                         --PGCEGMWDNI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:9207640; PIDN:AAA42331.1; PID:9207641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                Length 440;
                                                                                                                                                                                           Score 776; DB 2; Length 44; Pred. No. 1.6e-57; 64; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQ 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVOLEVOKKWOOWHL - - - - REFPLHPVASFSNSTKASHLEQSQ 432
                                                                                                                                                                                                                                                                                                                     39 WEEQDQCLQELSREQTGDLGT----EQPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translation not shown Molecule type: DNA
                                                                                   A;Cross-references: GDB:270546; OMIM:182098
A;Map position: 2q14.1-2q14.1
C;Superfamily: glucagon receptor
                                                                                                                                                                                             26.7%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JH0594
A; Molecule type: mRNA
A; Residues: 1-459 < ISH>
A; Cross-references: GB:M86835; NI
A; Experimental source: lung
B; Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A; Title: Characterization of the
A; Reference number: S56014; MUID:
                            Experimental source: pancreas
                                                                                                                                                                                                                                     Matches 177; Conservative
                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S56014
A; Status: prelimina
                                                                GDB:SCTR
                                                                                                                                                                                             Query Match
Best Local 3
                                              Genetics
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                                                                  A;Gene:
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Carrero, I.; Ogier-De

two cDNA

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A; Gene: GDB:VIPRI; RCDI; HVRI
A; Cross-references: GDB:128589; OMIM:192321
A; Cross-references: GDB:128589; OMIM:192321
A; Cross-references: GDB:128589; OMIM:192321
C; Map position: 3p22-3p22
C; Superfamily: glucagon receptor
C; Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein F:1-31, Commain: signal sequence #status predicted <SIG>F; 32-495/Product: vasoactive intestinal peptide receptor-related protein #status predicted F:180-203/Domain: transmembrane #status predicted <TML>F; 211-229/Domain: transmembrane #status predicted <TML>F; 251-269/Domain: transmembrane #status predicted <TML>F; 234-354/Domain: transmembrane #status predicted <TML>F; 391-398/Domain: transmembrane #status predicted <TML>F; 314-34/Domain: transmembrane #status predicted <TML>F; 314-34/Domain: transmembrane #status predicted <TMC>F; 314-43/Domain: transmembrane #status predicted <TMC>F; 314-35/Domain: transmembrane #status predicted <TMC>F; 314-36/Domain: transmembrane #status predicted <TMC>F; 314-86/Domain: transmembrane #status predicted <TMC>F; 314-36/Domain: transmembrane #status predicted <TMC>F; 314/Domain: transmembrane #status predicted <TMC>F
                                                 Ricouvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Blochem Biophys. Res. Commun. 200, 769-776, 1994
A.Title: Human intestinal VIP receptor: cloning and functional expression of A; Reference number: JC2194; MUID:94235025
A; Rocession: JC2194; MUID:94235025
A; Molecule type: mRNA
A; Residues: 1-495 < COU>
A; Residues: 1-495 < COU>
A; Residues: 1-605 < COU>
C; Courser references: EMBL:X7777; NID:9456352; PIDN:CAA54814.1; PID:9456353
C; Genetics: Courser feetences: jejunal epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ARSLLGS----SLQEECDYVQMIEVQHKQCLEEAQLENETIGCSKMWDNLTCWPATPRGQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ARAQLDSDGTITIEEQIVLVLKAKVQCELNI-TAQLQEGEGNCFPEWDGLICWPRGTVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 ISAVPCPPYIYDFNH---KGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ISIGKQE--FCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKO---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 755.5; DB 2
Pred. No. 9.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.0%;
Best Local Similarity 36.6%;
Matches 177; Conservative 8
                          C; Accession: JC2195; S42087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|:
AEVS 493
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Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A;Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal A;Reference number: PC2289; MUID:95118345
A;Accession: PC2289
A;Molecule type: mRNA
A;Residues: 63-129 <CCO>
C;Genetics: A;Gene: GDB:128589; OMIM:192321
A;Gene: GDB:VIPR1; RCD1; HVR1
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3922-3922
C;Superfamily: glucagon receptor
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane estatus predicted <TMID>
F;31-460/Product: vasoactive intestinal peptide receptor
F;14-168/Domain: signal sequence #status predicted <TMID>
F;16-234/Domain: transmembrane #status predicted <TMID>
F;16-234/Domain: transmembrane #status predicted <TMID>
F;25-277/Domain: transmembrane #status predicted <TMID>
F;25-277/Domain: transmembrane #status predicted <TMID>
F;26-234/Domain: transmembrane #status predicted <TMID>
F;346-363/Domain: transmembrane #status predicted <TMID>
F;36-30/Domain: transmembrane #status predicted <TMID>
F;36/Domain: transmembrane #status predicted <TMID>
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C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C.Accession: A53471, JU0185
R:Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.; Proc. Natl. Acad. Sci. U. S.A. 91, 2679-2683, 1994
A;Title: Cloning and functional characterization of a third pituitary adenylate cyclase-A;Reference number: A53471; MuID:94195806
A.Graphical A53471
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R;Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.
FEBS Lett. 334, 3-48, 1993
A;Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel A;Reference number: S39069; MUID:94039806
A;Moccession: S39069
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLVRVSSIHPECRFHLEIQEEETKCAELLSSQTENQRACSGVWDNITCWRPADVGETVTV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D28132; NID:9473721; PIDN:BAA05674.1; PID:9496376
A;Experimental source: strain C57BL/6
C;Superfamily: glucagon receptor
C;Keywords: receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.5%; Score 713.5; DB 2; Length 437; 33.6%; Pred. No. 2.8e-52; Live 87; Mismatches 156; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-437 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 33.69
Matches 163; Conservative
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GUZDZZZ

GUZDZZZ

CUZDZZZZ

CUZDZZZZ

CDBEC: 21 Dec.1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000

C; Accession: GOZBZ2; JC2463

R; Lutz, E.M.

Submitted to the EMBL Data Library, January 1996

A; Accession: GOZBZZ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-48 *LUTZ-

A; Cossolom, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr

A; Residues: Declamary; M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr

A; Residues: 1-48 *LUTZ-

A; Cossolom, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr

A; Toss-references: EMBL:X9509; NID:9110300

R; Svoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr

A; Title: Molecular cloning and functional characterization of a human VIP receptor fr

A; Molecule type: mRNA

A; Residues: 1-38 *T', 40-411, 'H', 413-423, 'A', 425-438 <SVO>

A; Coss-references: GB:335056; NID:9550477; PIDN:AAC37569.1; PID:9550478

A; Genetics:

A; Genetics:

A; Genetics:

A; Coss-references: GB:335025

A; Map position: 7436.3-7436.3

C; Superfamily: glucagon receptor: transmembrane #status predicted <TML>

F; 130-150/Domain: transmembrane #status predicted <TML>

F; 160-179/Domain: transmembrane #status predicted <TML>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 AVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398
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                                                                                                                                                                                                                                                                                                                                           41 VLKAKVQCELNITAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDF-NHKGVA 99
A;Cross-references: EMBL:Z25885; NID:g414188; PIDN:CAA81104.1; PID:g41418
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; intestine; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                       30 IQEEETKCAELLSSQM-ENHRACSGVWDNITCWRPADIGETVTVPCPKVFSNFYSRPGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 QNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 ILIGWGFPAAFVAAWAVARATLADARCWELSAGDIK-WIYQAPILAAIGLNFILFLNTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 LLIGWGIPSVCIGAWIATRESLEDTGCWDTNDHSIPWWVIRMPILISIVVNRALFISIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 VLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 437;
                                                                                                                                                                                         Query Match 24.4%; Score 708; DB 2; Length 43° Best Local Similarity 33.9%; Pred. No. 8.2e-52; Matches 159; Conservative 89; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPGSRDYRLHSWSMS-----RNGSES----ALQIHRGSRTQSFLQSET
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Job time:
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NiAlternate names: PACAP receptor
C; Species: Rattus norvegicus (Norway rat)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
A; Title: 03-Feb-1995 #NUD: 93326107
A; Residues: 1-467 CHOS>
A; Experimental source: brain
R; Speniler, D: Waeber, C; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; JC
Nature: 365, 170-175, 1993
A; Title: Differential signal transduction by five splice variants of the PACAP receptor.
A; Reference number: 336768; MUD: 93382505
A; Reference number: 336768; MUD: 93404252; PIDN: CAAB0817.1; PID: 9404253
C; Super: family: 91ucagon receptor
C; Keywords: alternative splicing; 91ycoprotein; receptor
C; Keywords: 115.299, 342, 374/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 77, 59, 116, 299, 342, 374/Binding site: carbohydrate (Asn) (covalent)
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F;206-228/Domain: transmembrane #status predicted <TM3>
F;241-262/Domain: transmembrane #status predicted <TM4>
F;282-304/Domain: transmembrane #status predicted <TM5>
F;329-349/Domain: transmembrane #status predicted <TM5>
F;329-348/Domain: transmembrane #status predicted <TM7>
F;56.88,92/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                SKNCTSDG-W-----SETFPDFVDACGYSDPE-DESKITFYILVKAIYTLGYSVSLMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILIGWGFPAAFVAAWAVARATLADARCWELSAGDIK-WIYQAPILAAIGLNFILFLNTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 LFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTP-PCGSRR---CGS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 438
                                                                                                                                                                                                                           Indels
                                                                                                                                                                           24.1%; Score 702; DB 2; Lk
36.1%; Pred. No. 2.6e-51;
ive 84; Mismatches 138;
                                                                                                                                                                                Query Match 24.15
Best Local Similarity 36.15
Matches 150; Conservative
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Length 467;

DB 2;

Score 696.5;

24.0%;

Query Match

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12;
                                                                                                       LNESSPGCPGMWDNITCWKPAQVGEMVLVSCPEVFRIFNPDQVWMTETIGDSGFADSNSL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 GWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNL----SVDWKRTPP--C
                                                                                                                                                ---HKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCE-RLYVMYTV
                                                                                                                                                                                                                                GYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKEL
                                                                                                                                                                                                                                                                                                                    ESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFF
                       75;
                       Indels
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    .3e-51;
es 149;
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                                                                LQEGEGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFN---
                       Mismatches
                       89;
  32.4%;
Best Local Similarity 32.49
Matches 150; Conservative
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Search completed: September 21, 2001, 17:06:31 Job time: 789 sec

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InterPro; IPR000832; -.
Pfam; PF00002; 7tm_2; 1.
PRINTS; PR00249; GPCRESCRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
GRFR_MOUSE
GLR_MOUSE
CALR_CAVPO
CALR_MOUSE
CALR_RAT
CALR_HUMAN
                                                                     CALR_PIG
CRF2_MOUSE
                                                             CRF1_CHICK
                                                       GRFR_RAT
                                                                                    CGRR_RAT
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                                                                                                                                                                                                                                                              MEDLINE=95318121; PubMed=7797535;
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EMBL; U47124; AAA96796.1; --
EMBL; U47125; AAC50767.1; --
EMBL; U47125; AAC50767.1; JOINE
EMBL; U47126; AAC50767.1; JOINE
EMBL; U47128; AAC50767.1; JOINE
EMBL; U47128; AAC50767.1; JOINE
EMBL; U47128; AAC50767.1; JOINE
EMBL; U47128; AAC50767.1; JOINE
                                                                                                                                                  STANDARD;
 Homo sapiens (Human).
200.5
200.5
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200.0
200.0
119.8
119.7
118.7
118.6
118.6
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P32215 r
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P41587
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                        93435 segs, 34255486 residues
                                                    September 21, 2001, 17:05:47
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PTRR_DIDMA
PTRR_PIG
PTRR_HUMAN
PTRR_MOUSE
SCRC_RAAT
SCRC_RABIT
VIPR_PIG
SCRC_HUMAN
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VIPS_RAT
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GLP2_RAT
GLP1_MOUSE
GIPR_MESAU
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PACR_MOUSE
PACR_BOVIN
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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gallus gall
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mus musculu
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"Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";
J. Biol. Chem. 270:13455-15458(1995).
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-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                           060755
P32214
P30988
P79222
Q02644
Q90812
P25117
Q60748
061606
                       008893
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01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).
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G_PROTEIN_RECEP_F2_2; 1.
G_PROTEIN_RECEP_F2_3; 1.
receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                      7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                         12;
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                             PARATHYROID HORMONE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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                        POTENTIAL.
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550 AA;
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MEDLINE-96426194; PubMed-8828488;

MEDLINE-96426194; PubMed-8828488;

MEDLINE-96426194; PubMed-8828488;

MEDLINE-96426194; PubMed-8828488;

Augin T.B., Bonner T.I., Harta G., Mezey E.;

Total in rat.";

Endocrinology 137:4285-4297(1996).

Control of parathyroid hormone-2 receptor messenger ribonucleic action of parathyroid hormone-2 receptor messenger ribonucleic action of parathyroid hormone. The action of parathyroid specific Receptor For Parathyroid Hormone. The Activity of THIS RECEPTOR IS MEDIATED BY G PROPEINS WHICH ACTIVATE ADDRIVITY CYCLASE. PTHRZ MAY BE RESPONSIBLE FOR PTH EFFECTS IN A NUMBER OF PHYSIOLOGICAL SYSTEMS. IT MAY PLAY A SIGNIFICANT ROLE IN PANCREATIC FUNCTION AS A NEUROPARANSMITTER RECEPTOR.

TISSUE SPECIFICITY: ABUNDANILY EXPRESSED IN BRAIN, ARTERIAL AND CARDIAC ENDOTHELIUM. FOUND AS WELL IN SPERM. IN THE HEAD OF THE EPIDIAMIS. LOWER EXPRESSION IS POUND IN VASCULAR SMOOTH MUSCLE, EXCERNE PANCREAS, TESTIS AND PLACENTA.

EXTINITARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch).
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                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCRDb; GCR_1413; -.
InterPro; IPR000832; -.
Pfam; PF00002; 7tm_2; 1.
PROSITE; PF000024; GPFSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00560; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS00560; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLESMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
                                      (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).
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RESULT

DB 1; Length 546;

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SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65963
                                                                                                                       PIR; A39286; A39286.
GCRDb; GCR_0204; -.
InterPro; IPR000832; -.
InterPro; IPR002170; -.
                                                                                                                                                                                                                                                                                                                                                                                 376
403
422
434
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585
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                                                                                                                      NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIH 180
                                                                                                                                MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV 240
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                                                                           61 GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
                                                                                                                                                                                                             VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT 300
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                                                                                                                                                                                                                                                                                                                                                                                           537
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Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E., Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr., Jr., Kronenberg H.M., Segre G.V.;
"A G protein-linked receptor for parathyroid hormone-related peptide.";
lormone-related peptide.";
science 254:1024-1026(1991).
-I-FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PRATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE DEDIVING.
CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
             Gaps
                                 9
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                                1 MAWLGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE
                                            481 SPA---DSLTATSLYLAMSGVTQSRTASHTLSTRSNKEDSGRQRDDILMEKPSRPMESNP
                                                                                                                                                                                                                                                                                                                                                                                                             478 TACROIDSHVTLPGYVWSSSEQDCQPQS---TPEETKKGHGRQEDDSPVGESSRPVAFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Didelphis marsupialis virginiana (North American opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                    LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTRR_DIDMA STANDARD; PRT; 585 AA.
P25107;
01-MAY-1992 (Rel. 22, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
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6
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
8.5e-164;
ches 82;
          37; Mismatches
  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRECURSOR (PTH/PTHR RECEPTOR)
 76.5%;
          Conservative
Best Local Similarity
Matches 416; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARATHYROID HORMONE/PARATHYROID HORMONE-
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24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPELAESAKDWMSRSAKTKKEKPAEK
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(YTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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PRINTS; PR00049; GTRECERETIN.

PRINTS; PR00393; PTRHORMONER.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; 1.

PROSITE; PS5027; G_PROTEIN_RECEP_F2_3; 1.

G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal.

SIGNAL 1 26
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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1.1e-100;
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CYTOPLASMIC (P
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PTRR_HUMAN
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                               321 FGWGLPAVFVAVWVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILFINIIRVLA 380
                                                              457
                                                                                                                    PARATHYROID HORMONE/PARATHYROID HORMONE-
                                                                                                        -STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED
                                                                         TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGCHYIVFVCLPHS-FTGLGWEIRMHCELF
                                                               FNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTH---
                                                                                                                                                                                                                                                                                                                        Euteleostomi;
Sus.
                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00002; 7tm_2; 1.

PRINTS; PR00249; GPCRSECREIN.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

G_PROTEIN_RECEP_F2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96305358; PubMed-8688470;
Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
Chandrasekhar S., Hsiung H.M.;
"Structure and functional expression of a complementary DNA for
porcine parathyroid hormone/parathyroid hormone-related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELATED PEPTIDE RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                         585 AA
                                                                                                                                                 SGRQRDDILM-----EKPSRPMESNPDT 539
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121 EVVAMPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLINETR--ERE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 ILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGD 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 VVHAHIGVKELESLIMQD-----DPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYW 253
                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                             5 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
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N-LINKED (GLORAC...) (POTENTIAL).
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01-OCT-1993 (Rel. 27, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
PRECURSOR (PTHA/PTHR RECEPTOR).
                                                                                                                                                                                                                                                                                                46.3%; Score 1345; DB 1; Length 585; 52.5%; Pred. No. 1.2e-96;
                                          3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                              Best Local Sim
Matches 259;
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TISSUE-Kidney;
MEDLINE-93238641; PubMed-8386612;
Schipani E., Karga H., Karga H., Karga H., Kronenberg H.M.,
Abou-Samra A.-B., Segre G.V., Jueppner H.;
"Identical complementary deoxyribonucleic acids encode a human renal
and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
Endocrinology 132:2157-2165(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOI. Enddorinol. 11:851-858(1997).

-i- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROFEINS WHICH ACTIVATE ADBRYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95263723; PubMed-7745008; Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F., Stuhrmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C., Brichman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M., Abou-Samra A.-B., Segre G.Y., Jueppner H., "Pseudohypoparathyroidism type Ib is not caused by mutations in the coding exons of the human parathyroid hormone (PTH)/PTH-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Constitutive activation of the cyclic adenosine 3',5'-monophosphate
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MEDLINE-95215874; PubMed=7701349;
Schipani E., Kruse K., Juppner H.;
A constitutively active mutant PTH-PTHrP receptor in Jansen-type metaphyseal chondrodysplasia.";
Science 268:98-100(1995).
                                                                                                                                                                                                                                                                                                            Schneider H., Feyen J.-H., Rao Movva N.; "Cloning and functional expression of a human parathyroid hormone
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96366745; PubMed-8703170; Schippani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S. Koob S.W., Colle W.G., Juppner H. "Constitutively activated receptors for parathyroid hormone and parathyroid hormone-related peptide in Jansen's metaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (XXX-1995) to the EMBL/GenBank/DDBJ databases.
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Blochemistry 37:12737-12743(1998).
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MEDLINE-98409426; PubMed-9737850;
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                                        NCBI_TaxID=9606;
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DR MIM; 168468; ...

DR MIM; 156400; ...

DR MIM; 2156400; ...

DR MIM; 2156400; ...

DR InterPro; IPR000832; -..

DR InterPro; IPR000170; -..

DR PRINTS; PR00019; Thm.2; PR00189; G_PROFILIN.

DR PRINTS; PR00199; G_PROFILIN.RECEP_F2_2; I.

DR PROSITE; PS00649; G_PROFILIN.RECEP_F2_2; I.

PROSITE; PS00649; G_PROFILIN.RECEP_F2_2; I.

PROSITE; PS005049; G_PROFILIN.RECEP_F2_2; I.

PROFILIN.RECEP_F2_2; I.

PROSITE; PS005049; G_PROFILIN.RECEP_F2_2; I.

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PROFILIN.RECEP_F2_2; I.

PROFILIN.RECEP_F2_2; I.

PROFILIN.RECEP_F2_2; I.

                                 -I-TISSUE SPECIFICATIVE EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN KIDNEY, BORE AND LIVER.
-I-DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF BLOMSTRAND TYPE OF CHONDRODYSPLASIA: A SPERE SKELETAL DISPLASYIA.
-I-DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF MUKK-JANSEN TYPE OF METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DISPLASYIA.
-I-DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF MUKK-JANSEN TYPE OF METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DISPLASYIA. IT IS A RARE FORM OF SHORT-LIMBED DWARRISM ASSOCIATED WITH HYPERCALCEMIA AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARATHYROID HORMONE/PARATHYROID HORMONE-
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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U22405, AAB60657.1; J
U22407, AAB60657.1; J
U22407, AAB60657.1; J
U22408, AAB60657.1; J
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PIR; A49191. A49191.
PDB; 1BL1; 30-MAR-99.
GCRDb; GCR_0205;
GCRDb; GCR_047; -.
GCRDb; GCR_1335; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PRATHYROID HORMONE-RELEPTOR
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                                                                                                      DB 1; Length 593;
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/FIId=VAR_003583.
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DA1400640A6C7F2B CRC64;
N-LINKED (GLCNAC. . .) (N-LINKED (GLCNAC. . .) (H -> R (IN MURK JANSEN;
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T -> P (IN MURK JANSEN;
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                                                                                                                                                                                                                                                                         Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F., Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.; "Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHR) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARATHYROID HORMONE/PARATHYROID HORMONE-
                   Abou-Samra A.-B., Jueppner H., Force T., Freeman M.M., Kong X.-F., Schippin E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr., Kronenberg H.M., Segre G.V.;
"Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: $ single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases intracellular free
                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED REPUTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADRIVLY CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00527; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 26
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
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MEDLINE-92212903; PubMed-1313566;
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GCRDb; GCR_0038; --
InterPro: IPR000032; --
InterPro: IPR002170; --
Pfam; PF00002; 7tm_2; --
PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00393; PTRHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M77184; AAA41811.1; -. EMBL; L19475; AAA68098.1; -.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              389 LGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRC 448
                                                                                                                                                                                                                                                                                                                                                                                                                  -SYGPMYSHTSVTNVGPRAG----LSLPLSPRLPP---ATTNGHSQLPGHAKPGAPATET 546
                                                                                                                        82 KASGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPLGAPGEVVAVPCPDYIYDFNHK 141
                                                                                                                                                   GVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISF 156
                                                                                                                                                                                                                                               260 ELHIIAQVPPPPAAAAVG----YAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAF 314
                                                                                                                                                                                                                                                                            FSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN 329
                                                                                                                                                                                                                                                                                       Gaps
                                                                     ----- 62
                                                                                200 ASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTLDEAERLTEE
                                                                                                                                                                                                                                                                                                                                                                          GSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESL---
                                                                                                                                                                                                                                                                                                                                                                                                     149 GSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSG-----VTQS
                                                                                                            ----IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAF
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karperien M., van Dijk T.B., Hoeijmakers T., Cremers F., Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.; Expression pattern of parathyroid hormone/parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes."; Mech. Dev. 47:29-42(1994).
                                                  87;
                             DB 1; Length 591;
                                                                    22 ARAQLDSDGTITIEEQIVLVLKAKVQCE-----LNITAQLQEGEGN----
                                                 86; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTRR_MOUSE STANDARD; PRT; 591 AA.
P41593; 062119;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE
66260 MW; 21944F3051B9E9C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             502 RTASHTLSTRS-----NKEDSGRQRDDILMEK 528
                            Score 1331.5; DB Pred. No. 1.3e-95;
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MEDLINE-95034305; PubMed-7524627;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                            45.8%;
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PTHR1 OR PTHR.
                                                 Matches 270; Conservative
591 AA;
                                        Similarity
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SEQUENCE
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                                        Local
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SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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MEDLINE-9425468; PubMed-8197183;
McCuaig K.A., Clarke J.C., White J.H.;
Proc. Natl. acad. sci. U.S.A. 91:5051-5055(1994).
-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELARDE PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL.
CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
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R GCRD; GCR_1614; ...
R InterPro; 1PR000832; ...
R InterPro; 1PR00170; ...
R Pfam; PF00002; 7tm_2; 1...
R PRINTS; PR00149; GPCRSECRETIN.
R PRINTS; PR00649; G_PROTEIN_RECEP_F2_1; 1.
R PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
R PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
R PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
R G_PROTEIN_RECEP_F2_2; 1.
R G_PROTEIN_RECEP_F2_3; 1.
R G_PROTEIN_RECEP_F2_3; 1.
T SIGNAL 26 PROTEIN_RECEP_F2_3; 1.
T SIGNAL 27 S91 PARATHYROID HORMONE/PARATHYROID HORMONE
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N-LINKED (GLCNAC. . .) (POTENTIAL).

DA -> TS (IN REF. 2).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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F7876F8D388BDDFD CRC64;
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6 (POTENTIAL).
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EMBL; L34611; AAA40011.1; -.
EMBL; L34608; AAA40011.1; JOINED.
EMBL; L34607; AAA40011.1; JOINED.
EMBL; L34609; AAA40011.1; JOINED.
EMBL; L34610; AAA40011.1; JOINED.
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Best Local Similarity 52.4
Matches 250; Conservative
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GCRDb; GCR_1614;
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                                                                   141
 62
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Sciurognathi; Muridae; Murinae; Rattus
                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THIS
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SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                          389 LGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGS 445
                                                                                                                                                                                                                                                                                                                                        GVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISF
                                                                                                                GHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMTNETR - - EREVFDRLGMIYTVGYSMSL
                                                                                                                                     GSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESL---
                                                                                                                                                  200 ASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTLDEBERLTEE
                                                                                                                                                                                               FSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN
                                                                                                                                                                                                                                                                               FILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVLVFGVHYIVFVCLPHS-FTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagata S., \mbox{\sc "Molecular} cloning and expression of a cDNA encoding the secretin
                                            -----CFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-91266890; Pubmed-1646711;
Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0. 10:1635-1641(1991).
FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 ARAQLDSDGTITIEEQIVLVLKAKVQCE----LNITAQLQEGEGN-
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-RPR-1993 (Rel. 25, Last annotation update)
SECRETIN RECEPTOR PRECURSOR (SCT-R).
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Mammalla, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X59132; CAA41849.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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InterPro; IPR000832; -.
InterPro; IPR002144; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 LMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQL-QEGEGNCFPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LILRILLLTKAA----HTVGVPPRLCDVRRVLLEERAHCLQQLSKEKKGALGPETASGCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 IGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSII
                                          PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS06650; G_ROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                      -LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 801; DB 1; Length 449;
Pred. No. 9.5e-55;
81; Mismatches 149; Indels
                                                                                                                                                                                                                                                         4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                        SECRETIN RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                          6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYDOLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (P
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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          PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00490; SECRETINR.
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ME
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37.38;
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Matches 176; Conservative
Pfam; PF00002; 7tm_2; 1.
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046502;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                        "Molecular cloning and in vitro properties of the recombinant rabbit
                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLEASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                           Vertebrata; Euteleostomi;
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.

SIGNAL 1

21

POTENTIAL.
                                                                                                                                                                                                                                                                            Svoboda M., Tastenoy M., de Neef P., Delporte C., Waelbroeck M.,
Robberecht P.;
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CYTOPLASMIC (POTENTIAL).
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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EXTRACELLULAR (POTENTIAL)
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                          Last sequence update)
Last annotation update)
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. 38, Created)
. 38, Last sequence uplaced and the sequence uplaced and
                                                                                                                                                                                                                                                    MEDLINE=98366112; PubMed=9700755;
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InterPro; IPR000832; -.
InterPro; IPR001771; -.
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PRINTS; PR00490; SECRETINR.
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                                                                                                                                                                                                                                                                                                                                             secretin receptor.";
Peptides 19:1055-1062(1998).
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445 AA;
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                                                                   SECRETIN RECEPTOR
                          (Rel.
                                                Rel
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15-JUL-1999 (
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
(PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
                                                                  107
                                                                                                   163
                                                                                                                                                                    223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --WDGLICWPRGTVGKISAVPCPPYIYDF-NHKGVAFRHCNPNGTWDFMH 113
                                                                                                                                  -----WTE-----TFPRPDLACGVSMNDSSHERQHAYLLKLKVMYTVGYSSSLVMLLVAL 157
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                        224 EATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIG
                                                                                                                                                                                                                                                            WGFPAAFVAAWAVARATLADARCWELSA-GDIKWIYQAPILAAIGLNFILFLNTVRVLAT
                                                                                                                                                                                                                                                                                                                               --LVGAPPRLCD--VLWVLQEERDQCLQELERERL
                                                      GEEQPVPGCQGLWDNVSCWPSSAPGRWVELECPRFLRMLTNSNGSLFRNCTQDG-----
                                                                                                   SLNKTWANYSDCLRFLQPDISIG------KQEFCERLYVMYTVGYSISFGSLAVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVL-TTVTHSTSS
                                                                                                                                                                    164 LIIGYFRRLHCTRNYIHMHLEVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Hsiung H.M., Smith D.P., Hyslop P.A., Heiman M.L., Hassan H.A.,
Zhang X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PACAP TYPE II RECEPTOR) (PACAP-R-2). VIPR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U49434; AAA93390.1; -. GCRDb; GCR_1565; -. InterPro; IPR000832; -. InterPro; IPR001571; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
WLLLGFACAAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 LNSTKA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 QSQVAA 467
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Q28992;
                                                                                                                                                                                                                                                                                                           284
                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
                                67
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17;

Gaps

98;

27.3%; Score 794; DB 1; Length 445; 37.4%; Pred. No. 3.3e-54; ive 71; Mismatches 135; Indels

Conservative

Similarity

Query Match Best Local Simi Matches 182;

ò

13 WIMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNCFPE----- 66

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18;
                                                                                                                                                                                                                                                                                                                                                                                                                                        228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 PEWDGLICWPRGTVGKISAVPCPPYIYDFN-HKGV-AFRHCNPNGTWDFMHSLNKTWANY 122
                                                                                                                                                                                                                                                                                                                                                                                                      123 SDCLRFLQP-----DISIGKQE----FCERLYVMYTVGYSISFGSLAVALLIIGY 168
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                             10 GWF----CVLAGVLACVLGPVGSWAVGLQQEECDYLQMIKVQHKQCLEEAQLENETSGCS 65
                                                                                                                                                                                                                                                                                                                                   GWLMLGSCLLA---RAQLDSDGTITI---EEQIVLVLKAKVQCELNI-TAQLQEGEGNCF 64
                                                                                                                                                                                                                                                                                                                                                                                      66 KMWDNLTCWPATPRGQVVVLACPLIFKLFSPTQGLNVSRNCTDEG-------WTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                        FRRLHCTRNY IHMHLEVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

E166E4D6B3BE1189 CRC64;
                                PRINTS; PRO1154; VIPIRECEPTOR.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.

SIGNAL

POTENTIAL.
                                                                                                                                                                                                                                                                                                                 82;
                                                                                 VASOACTIVE INTESTINAL POLYPEPTIDE
                                                                                                                                                                                                                                                                                                  Length 458;
                                                                                                                                                                                                                                                                                                27.0%; Score 785; DB 1; Length 450
37.0%; Pred. No. 1.7e-53;
.ive 76; Mismatches 152; Indels
                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                 3 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                   (POTENTIAL)
                                                                                              RECEPTOR :
InterPro; IPR001771; -.
Pfam; PF00002; 7fm_2; 1.
Prinrs; PR00249; GPCRECETIN.
PRINTS; PR00491; VASOACTVEIPR.
                                                                                                                                                                                                                                                                        Ψ.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.0%
Matches 182; Conservative
                                                                                                                                                                                          342
362
374
394
458
59
70
101
51479
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ARRSSSFQAEVS 456
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105
458 AA;
                                                                                                      DOMAIN
TRANSMEM
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TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                     Jiang S., Ulrich C.D.; ^{\mathtt{MOlecular}} cloning and functional expression of a human pancreatic
                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Homin1dae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000832; -.
InterPro; IPR002144; -.
Pfam; PF00002; 7tm_2: 1.
PRINTS; PR00409; GPCRSECRETIN.
PRINTS; PR00409; SECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00227; G_PROTEIN_RECEP_F2_2: 1.
G_PROTEIN; PS0227; G_PROTEIN_RECEP_F2_3: 1.
G_PROTEIN COUPLED CEPPER COUNTAIN.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chow B.K.-C., ^{\prime} "Molecular cloning and functional characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 212:204-211(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                       secretin receptor.";
Biochem. Biophys. Res. Commun. 207:883-890(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
SECRETIN RECEPTOR
SCRC_HUMAN STANDARD; PRT; 440 AA. P47872; Q13213; Q12961; 01-FEB-1996 (Rel. 33, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) SECRETIN RECEPTOR PRECURSOR (SCT-R).
                                                                                                                                                                                                                                                                                                                                     TISSUE=Pancreas;
MEDLINE=95169147; PubMed=7864894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95336443; PubMed=7612008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U20178; AAC50106.1; -. EMBL; U28281; AAA87556.1; -. EMBL; U13989; AAA64949.1; -. GCRD; GCR_1995; -. GCRD; GCR_2016; -.
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143
167
174
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MIM; 182098; -.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Pancreas
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TRANSMEM
DOMAIN
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Interpro; IPR000832; --
Pfam; PF00002; 7tm,2; 1.
PRINTS; PR00249; GPCRSECRETIN.
PROSITE; PS00649; G_PROTEIN RR
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22
64
91
169
50959 B
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Best Local Similarity 35.09
Matches 165; Conservative
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1135
1155
1178
1202
202
202
203
305
305
337
447
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 TLADARCWELSA-GDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICWPRGTVGKISAVPCPPYIYDF-NHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPDISIG------KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::::| :::| :::| :::| :::| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 WEEQDQCLQELSREQTGDLGT----EQPV--------PGCEGMWDNI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR).
Carassius auratus (Goldish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARA
                                                                                                                                                        7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
A -> P (IN REF. 1).
A -> P (IN REF. 2).
I -> F (IN REF. 3).
C -> A (IN REF. 3).
G -> A (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 784; DB 1; Length 440;
; Pred. No. 1.9e-53;
64; Mismatches 138; Indels
                                                                            EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
               EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            E22CDD0EE7C0ACC1 CRC64;
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                                                                                                                                                                                                                                                                        | -> A (IN REF. 1).
| -> P (IN REF. 2).
| -> F (IN REF. 3).
| -> Q (IN REF. 3).
| -> A (IN REF. 1).
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                                                                (POTENTIAL)
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38.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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100
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128
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124
124
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318
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308
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Q90308;
01-NOV-1997 (
                                               DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                        MEDLINE=97190233; PubMed=9038250;
Chow B.K.C., Yuen T.H., Chan K.W.,
Chow B.K.C., Yuen T.H., Chan K.W.,
"Molecular evolution of vertebrate VIP receptors and functional
characterization of a VIP receptor from goldfish Carassius auratus.";
Gen. Comp. Endocrinol. 105:176-185(1997).
-I- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AKVQCELNITAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDF--NHKGVAFR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 HCNPNGTWDFM-----HSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TCTADG-WTEMDPMEIAVYCGYNLNGT------VDDDSFFRSVKIGYTIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271
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                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 YSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLIMODDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFS
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00649, G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00669; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00277; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 103 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
Cypriniformes; Cyprinidae; Cyprininae; Carassius NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                   272
                                                                               389
                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1997 (Rel. 25, Last annotation update)
VASOACTIVE INTESTIRAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
(PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
(PAGAP TYPE II RECEPTOR) (PACAP-R-2).
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel receptor
 DVIQESD--NCSTAS-----VGCKAVIVFFQYCIMASFFWLLVEGLYLHALLAVSFFS
                                        |:|: :\ ||||| |:::||: |||||||:|
KTELRLVFDLILGSFQGFVVAVLYCFLNGEVQAEIKRKWRRWHLERFLGPDTKYQHPSMG
                         DTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWEL--SAGDIKWIYQAPILAAIGLN
                                                                             FILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO002; 7tm_2; 1.

PRINTS; PR00029; GFCRECRETIN.

PRINTS; PR00191; VASOACTVEIPR.

PRINTS; PR01054; VIPIRECEPPOR.

PROSITE; PS00659; G_PROTEIN_RECEP_F2_1; 1.

PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

PROSITE; PS0027; G_PROTEIN_RECEP_F2_3; 1.

G-PROTEIN_RECEP_F2_3; 1.

G-PROTEIN_RECEP_F2_3; 1.

G-PROTEIN_RECEP_F2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                      -----SVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAAAH 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagata S.;
a novel re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 8:811-819(1992).
                                                                                                                                                                                                                389 SNGNNFSTQISMLTRCSPKTRRASTCQDETSITVLGSTTMGYGHQNETVKGH
                                                                                                                                 GWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishihara T., Shigemoto R., Mori K., Takahashi K., "Functional expression and tissue distribution of for vasoactive intestinal polypeptide.";
                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                   459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Lung;
MEDLINE-92232309; PubMed-1314625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M86835; AAA42331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JH0594; JH0594.
GCRDb; GCR_0369; -.
InterPro; IPR000132; -.
InterPro; IPR001571; -.
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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30-MAY-2000 (Rel. 39, Last annotation update)
40-MASOACTIVE INTESTIRAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
(PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 EQIVLVLKAKVQCELNITAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCP-----PY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || :|||| :| :||:||: :|| |: :|| LWWIIKAPILLSILVNFVLFICIIRILVQKLRPPD-IGKNDSSPYSRLAKSTLLLIPLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYLQLIEIQRQCCLEE -- AQLENETTGCSKMWDNLTCWPTTPRGQAVVLDCPLIFQLFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 IYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQP---DISIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IHGYN----ISRSCTEEG------WSQ------LEPGPYHIACGLNDRASSLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMMSRWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWI
                                                                                                                                        4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

TO (POTENTIAL).

TO (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               83;
VASOACTIVE INTESTINAL POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S--VDW--KRTPPCGSRR---CG---SVLTTVT----HSTSSQSQVA 466
                                                                            2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                              EXTRACELLULAR (POTENTIAL)
                                                               (POTENTIAL).
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Pred. No. 1.5e-52;
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                                               1 (POTENTIAL)
CYTOPLASMIC (1
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36.8%; Pred
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01-007-1993 (Rel. 27, Created)

01-007-1993 (Rel. 27, Last seq

30-MAY 2000 (Rel. 39, Last ann
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52057
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Best Local Similarity
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                                                                                                                                                                                                   Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I., Ogier-Denis E., Laburthe M.;
"Human intestinal VIP receptor: cloning and functional expression of two CDNA encoding proteins with different N-terminal domains.";
Biochem. Biophys. Res. Commun. 200:769-776(1994).
                                                                                                                                                                                                                                                                                                                            Gagnon A.W., Aiyar N., Elshourbagy N.A.; "Molecular cloning and functional characterization of a human liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS, RAJI B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY, LIVER AND PLACENTA.

SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    vasoactive intestinal peptide receptor.";
cell. Signal. 531-33(1994).
-!- FUNCTION: THIS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE. THE AFFINITY IS VIP - PACAP-27 > PACAP-38.
-!- SUBCELLULAR LOCATION: TWO FORMS ARE PRODUCED BY ALTERNATIVE
                                                                                          Sreedharan S.P., Patel D.R., Huang J.-X., Goet2l E.J.; "Cloning and functional expression of a human neuroendocrine vasoactive intestinal peptide receptor."; Biophys. Res. Commun. 193:546-553(1993).
                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                 TISSUE-Intestine;
MEDLINE-93290641; PubMed-8390245;
                                                                                                                                                                                        MEDLINE-94235025; PubMed-8179610;
                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
MEDLINE-95001220; PubMed-7917790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U11081; AAB60362.1; JOINED.
U11083; AAB60362.1; JOINED.
U11084; AAB60362.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U11085; AAB60362.1; JOINED.
EMBL; U11086; AAB60362.1; JOINED.
EMBL; L13288; AAA36805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00002; 7tm 2; 1.
PRINTS; PR00249; GPCRSECRFIN.
PRINTS; PR01491; VASOACTVEIPR.
PRINTS; PR01154; VIPIRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X77777; CAA54814.1; -. EMBL; X75299; CAA53046.1; -. EMBL; L20295; AAA36802.1; -. PIR; JN0604; JN0604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U11087; AAB60362.1; -. EMBL; U11079; AAB60362.1; JO EMBL; U11080; AAB60362.1; JO
                                                                                                                                                                                                                                                                                    SEQUENCE OF 33-457 FROM N.A.
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GCRDb, GCR_0652,
GCRDb, GCR_0774,
GCRDb, GCR_0904,
                                                   SEQUENCE FROM N.A.
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                          NCBI_TaxID=9606;
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EMBL;
EMBL;
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DAA40CF5BEC47D7D CRC64;
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS5027; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
SIGNAL 1 30
VASOACTIVE INTESTINAL POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.1%; Score 759.5; DB 1; 36.2%; Pred. No. 1.6e-51; ive 80; Mismatches 145;
                                                                                                                                                           (POTENTIAL)
                                                                                                                      RECEPTOR
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Best Local Similarity 36.2
Matches 179; Conservative
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Search completed: September 21, 2001, 17:08:50
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                                       VIDE_MOUSE STANDARD; PRT; 437 AA.
P4158B; P97750;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-YOUNG (Rel. 40, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2)
(PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)
(PACAP TYPE III RECEPTOR) (PACAP-R-3).
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C; TISSUE-Thymus; MEDLINE-96378694; PubMed-8784257; Delgado M., Martinez C., Johnson M.C., Gomariz R.P., Ganea D.; "Differential expression of vasoactive intestinal peptide receptors 1 and 2 (VIP-R1 and VIP-R2) mRNA in murine lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Neuroimmunol. 68:27-38(1996).

-I-FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27, THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENIXIZ CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.

-I-SUBGEELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-I-TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE MING CELLS, AT MODERATE LEVELS IN PANOREATIC ISLETS, INSULIN-SECRETING CELLS, LING, BRAIN, STOMACH, AND COLON, AND AT LOW LEVELS IN THE HEART.

-I-SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPPORS.
                                                                                                                                                                                                                                                                                     MEDLINE-94195806; PubMed-8146174;
Inagaki N., Yoshida H., Mizuta M., Mizuno N., Fujii Y., Gonoi T.,
Miyazaki J.-I., Seino S.;
"Cloning and functional characterization of a third pituitary
adenylate cyclase-activating polypeptide receptor subtype expressed
in insulin-secreting cells.,
Proc. Natl. Acad. Sci. U.S.A. 91:2679-2683(1994).
                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0249; GPCRSECRETIN.
PRINTS; PR00491; VASOACTVEIPR.
PRINTS; PR01155; VIPZRECEPTOR.
PROSITE; PS00669; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G_PTOTEIN COUPLED F2_2; 1.
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1 (POTENTIAL)

CYTOPLASMIC (POTENTIAL)
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6 (POTENTIAL).
EXTRACELLOLAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
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; Pred. No. 5.3e-48;
87; Mismatches 156; Indels 79
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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5 (POTENTIAL).
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CCC870A094F9DC90 CRC64;
                                                 4 (POTENTIAL)
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Best Local Similarity 33.6%;
Matches 163; Conservative 87
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O70440 mus musculu rattus norv rattus norv rattus norv bos taurus bos taurus homo sapien homo sapien

Q92174 088917 088923 09har3 094910 1

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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MEDLINE-99367425; PubMed=10438471;
Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
"A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of J. Biol. Chem. 274:23035-23042(1999).
EMBL; AFI32082; AAD51988.1; -.
InterPro; IPR001879; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostarlophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                 Q9WUP2
Q9QXH8
Q9R1W5
Q9V716
Q9V6C7
O57671
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Q98955
Q9YHC8
Q9U3P6
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Q9PWB7
09yhc6 rana ridibu
09r1t8 mus musculu
09ji40 mus musculu
09jb92 gallus gall
073769 carassius a
09ptk1 xenopus lae
09ptk1 xenopus lae
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                                                                                                                 ; Search time 27.61 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd
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Gaps

DB 13; Length 575;

watch 57.7%; Score 1677.5; DB 13; Lengt Local Similarity 60.8%; Pred. No. 1.6e-131; Lengt as 322; Conservative 72; Mismatches 109; Indels

Query Match

Best Loca Matches

Ogniff bos taurus Ogtujo bos taurus Ogtuji bos taurus Ogwug9 rattus norv Ogpuki hoplobatrac

09W099 Q9PUK1 Q9GMD1 Q9HB45

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604 592 566.5 554

Q9TUJ0 Q9TUJ1 **09N1F8**

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Result

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MEDLINE-99428481; PubMed-10497171;
Rubin D.A., Jueppner H.;
Rubin D.A., Jueppner H.;
Rebrafish Express the Common Parathyroid Hormone-/Parathyroid Hormone-related Peptide Receptor (PTHIR) and a Novel Receptor (PTH3R) That Is Preferentially Activated by Mammalian and Fugufish Parathyroid Hormone-related Peptide.";
D. Biol. Chem. 274:28185-28190(1999).
EMBL; AF132084; AAF01265.1; -.
HSSP; Q03431; 1BL1.
InterPro; IPR000832; -.
InterPro; IPR001899; -.
Pfam; PF00002; 7tm_2; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROLD HORNONDE RECEPTOR FTHIR.
Brachyddanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil: Neopterygil; Teleostel; Euteleostel; Ostarlophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                            265 IFVAFFSDTKYLWGFILLIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILA
                                                                                                                                                   AIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFVFGVHYIVFVCLPH
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        PCPPY IYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY SDCLRFLQPDISIGKQEFCERL
                                                  YVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAH
                                                                                            205 IGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNL
                                                                                                                                                                                                                                                                                                               540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.8%; Score 1418.5; DB 13; Length llarity 57.8%; Pred. No. 5.3e-110; Conservative 80; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                          505 S---HTLSTRSNK-----EDSGRQRDDILMEK--PSRPMESNPDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61454 MW; 653B0A56DB2C8FA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       536 AA
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Simi
Matches 269;
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SEQUENCE
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                                                                                                         240 TLELYFLATNYWILVEGLYLHSLIFMTFFSDRKYLWGFTLIGWGVPAMFVTIWASVRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   LADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGASLHV -- WGWLMLGSCL - LARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE
                        :||:||:| | |:| |: | :: : | MGATLIVRTLGFLEFCGTLLSFVYGLVDADDVLTKEEOIYLLFNAKRKCERAIKSKHKTSE
                                                                                   GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA
                                                                                                                                                                                                                                                                                                                                             24.1 VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGE
                                                                                                                                                                                                                                                            MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
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Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.; "Molecular cloning and functional characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.3%; Score 1345.5; DB 6; Length Best Local Similarity 46.5%; Pred. No. 7.2e-104; Matches 281; Conservative 90; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parathyroid hormone receptor-1 (PTH1).";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF167095; AAD55938.1; -.
HSSP; Q03431, 1BL1.
InterPro: IPR000832; -.
InterPro: IRR00879; -.
Pfam: PF00002; 7tm_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 VQAEVKKMWSRWNLSVDWKRTPPCGSR--RCGSVL--TTVTHSTS 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09568ECF38D4D258 CRC64;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE RECEPTOR-1.
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SEQUENCE
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08688658E2727303 CRC64;

61438 MW;

542 AA;

SEQUENCE

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SEQUENCE FROM N.A.

MEDLINE-99428481; PubMed=10497171;

Rubin D.A., Jueppner H. O.,

Rubin D.A., Jueppner H. O.,

"Zebrafish Express the Common Parathyroid Hormone-/Parathyroid Hormone-related Peptide Receptor (PTHIR) and a Novel Receptor (PTHIR) That Is preferentially Activated by Mammalian and Fugufish Parathyroid Hormone-related Peptide.";

J. Biol. Chem. 274:28185-28190(1999).

BMBL, PARI32085, AAF01266.2;

InterPro; IPR000832;

InterPro; IPR001879;
                                                                                                                     61 DIMESDKGWASASTSGKPKKEKASGKLYPESEEDKEVPTGSRHRGRPCLPEWDHILCWPL 120
                                                                                                                                                                                                                                                                                    249 TNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVL 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPRSPADSLT 487
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cyptiniformes; Cyprinidae; Rasborinae; Danio.
OSL TAXID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CFPEWDGLICWPR
                                                                                                                                                                                                                                                   136 GKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIHMHLFVSFMLRATSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 WSRWTLALDFKRKARSGSSSY-SYGPMVSHTSVTNVGPRAGLGLPLSPRLLPAAATTTA
                                                                                                                                                                                                                                                                                                                                                                            196 VKDRVVHAHIGVKELESL-----IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLA
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE RELATED PROTEIN RECEPTOR PTH3R.
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---EGEGN-
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Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
"A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of 21 sioun-regulating peptide hormones.";
J. Biol. Chem. 274:23035-23042(1999).
InterPro; IPR000832;
                                                                                                                   76 GTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISI 135
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                                Gaps
                                                          75
                                                                                       73
                                                                                                                                                                                                                                                        19 CLL--ARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQ-EGEGNCFPEWDGLICWPR
                                                                           136 GRQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIF
                                                                                                                                                                                            VKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWIL
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                               256 VEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIK
                                                                                                                                                                                                                                                                                                                                                         316 WIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVFGVH
                                                                                                                                                                                                                                                                                                                                                                                                                  376 YIVFVCLPHS-FTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLS
   542;
                              65;
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 Length
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
; Score 1307.5; DB 13; Lengt; Pred. No. 9.4e-101; B4; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 LDLKQKARVHSSAGCGSGYYGGMM---SHTTTQ-------
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 45.0%;
                             Matches 260; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (Mouse).
                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 AA;
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hes 181;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
                                                                                                                                                  250 NYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWEL 309
                                                                                                                                                                                                                                         SAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 IYDFNH---KGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQE-FCERLY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
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----SVGCKAAMVFFQYCIMANFFWLLVEG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                              Gaps
                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-mar-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASOACTIVE INTESTINAL PEPTIDE/PITUITARY ADENYLATE CYCLASE ACTIVATING
POLYPEPTIDE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ILCVPEECSIMYQIELKHEECVNHEDYFNDTAVCKRTWDNITCWPSASIGEVVVLQCPGY 76
                                                                                                                                                                              VLKAKVQCELNITAQLQEGE------GNCFPEWDGLICWPRGTVGKISAVPCPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---HAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana ridibunda (Laughing frog) (Marsh frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVV ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexandre D., Anouar Y.; A cloned frog VIP/PACAP receptor exhibits pharmacological and distribution characteristics of both VPAC1 and VPAC2 receptors
                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                  Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%; Score 814; DB 13; Length 444; 36.8%; Pred. No. 9.2e-60; ive 73; Mismatches 133; Indels 8:
                                                                                                                                                                                                                                                                                                                                                       120 LVFGVHYIVFVCQPHSFSGLWWEIRMHCELFFNSFQGFFVSIIYCFCNGE 169
                                                                                                                                                                                                                                                                                                                                 LVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGE 419
                                                                                                           Indels
  748CC8231F1C69EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883B25B729314C4C CRC64;
                                                                  DB 11;
                                                                                                       7;
                                                                Score 858.5; DB Pred. No. 6e-64;
                                                29.5%; Sco. 10. 00. 92.9%; Pred. No. 00. 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00249; GPCRSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
SWART; SM00008; Horms; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 AA; 50955 MW;
19674 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF100644; AAD03602.1;
InterPro; IPR000832; -.
InterPro; IPR01879; -.
Pfam; PF00002; 7tm_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.88
Matches 168; Conservative
                                                                                Local Similarity 92.9
nes 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrinology 0:0-0(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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  169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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  SEQUENCE
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                                                                  Query Match
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                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
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                                                                                                                                                                                                     65 PEWDGLICWPRGTVGKISAVPCPPYIYDFN--HKGVAFRHCNPNGTWDFMHSLNKTWANY 122
                                                                                                                                                                                                                                                                                                                                                FVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNL----S 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 WLMLGSCLLARA---QLDSDGTITIE-----EQIVLVLKAKVQCELNITAQLQEGEGNCF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hashimoto H., Nishino A., Shintani N., Hagihara N., Copeland N.G., Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
319 QAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.2%; Score 791.5; DB 11; Length 459; 36.6%; Pred. No. 7.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE 1 (VPAC1) RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>..</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 KDMKYHHPSLGSNGTNFSTQISMLTKCSPKTRRCSS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERLIA SO 23 (1993); CONTROLL SO 23 (1994); C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=129SVJ;
MEDLINE=99265976; PubMed=10331949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00008; HormR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000832;
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D 65 KAWDNLTCWPTTPWGQVVVLDCPLIFQLFSPIHGYNISRNCTEEGWS	WSQ- 112		65 KMWDNLTCWPTTPWGOVY
123 SDCLRFLQPDISIG	AILIIG 167 : : AMAILS 166	٠, ٦	SDCLRFLQPDISIG-
Y 168 YFRRLHCTRNYIHMHLEVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATS	SIEATS 227 : CSEAS- 213	113	113LEPGPYHIACGI 168 YFRELHCTRNYIHMHLFV
y 228 VDKSQYIGCKIAVVMFIYFLATNYYMILVEGLYLHNLIFVAFFSDTKYLMGFILIGWGFP :	IGWGFP 287 IGWGVP 267		LFRKLHCTRNYIHMHLEN VDKSQYIGCKIAVVMFIN :
y 288 aafvaawavaratladarcwe-lsagdikwiyqapilaaiglnfilelntvrvlatkiwe :	ATKIWE 346 : VQKLRP 327	214	VSCKAAVVEFQ) AAFVAAWAVARATLADAF
y 347 TNAVGHDTRQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQG :: :	FNSFQG 406 VGSFQG 383	DD 268 SVFI QY 347 TNAV	SVFIMIWTIVRIHFEDEC TNAVGHDTRKQYRKLAKS
19 407 FFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPPGGSRRGGSVLTTVT	VLTTVT 456 : : MLTRVS 443	407	FFVSIIYCYCNGEVQAEY
<pre>/y 457HSTSSQSQVA 466 </pre>		384	384 FVVAILYCFLNGEVQAEI 457HSTSSQSQVA 46(: :: :
RSCIII.79 A		Db 444 PSAF	RSSSFQAEVS 45
795140 TD 095140 PRELIMINARY; PRT; 459 AA.		SUL	
<pre>XC Q9J140; yr Ol-OCT-2000 (TrEMBLrel. 15, Created) yr Ol-OCT-2000 (TrEMBLrel. 15, Last sequence update) yr Ol-MAR.2001 (TrEMBLrel. 16, Last annotation update) br VASOACTIVE INTESTINAL PEPTIDE RECEPTOR TYPE 1.</pre>			091BG2 991BG2, 01-0CT-2000 (TrEMBLrel 01-0CT-2000 (TrEMBLrel 01-MAR-2001 (TrEMBLrel
<pre>SN VIPR1. SN Wus musculus (Mouse). CD Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi; CD Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NN NCRI TAYID=10090.</pre>	stomi; e; Mus.		VASOACTIVE INTESTINAL CVIPR. CVIPR. Gallus gallus (Chicken Eukaryota; Metazoa; Ch
	ide d Murine		Gallus. NCBL_raxID=9031; [1] SEQUENCE FROM N.A. Kansaku N., Shimada K.
			"Molecular cloning of and chromosomal locali Submitted (JUL-1999) to FMRT: AB0298951
		DR InterPro DR InterPro DR Pfam; PF	InterPro; IPR00083; InterPro; IPR001879; Pfam; PF00002; 7tm_2; PRINTS; PR00249; GPCRS
SMART; SM00008; HOTMR; 1. Receptor. SEQUENCE 459 AA; 52095 MW; 9D1ADFB85			PROSITE; PS00650; G_PR SMART; SM00008; HormR; Receptor. 1
Query Match 27.2%; Score 791.5; DB 11; Length 459; Best Local Similarity 36.6%; Pred. No. 7.1e-58; Matches 181; Conservative 81; Mismatches 145; Indels 87;	59; 87; Gaps 19;	Sue	418 AA; 48
OY 13 WLMLGSCLLARAOLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNCF 64	SGEGNCF 64	Match	es 166; Conservati
UD 11 WLTT-CVIEWGALACALGERGSFRUELEILUMIENVRUCLEET-AUEREITUGGS 04 OY 65 PEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 122	METICOS 04 MKTWANY 122	27 32 1115. 	SEERSOC

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n).
hordata; Craniata; Vertebrata; Euteleostomi;
ognathae; Galliformes; Phasianidae; Phasianinae;
VVVLDCPLIFQLESPIHGYNISRNCTEEG------WSQ-112
                                                                                                                                       213
                                                                                                                                                                                                                                                                                                                      EVKKMWSRWNLS--VDW--KRTPPCGSRR---CG---SVLTTVT 456
                                           S------KQEFCERLYVMYTVGYSISFGSLAVAILIIG 167
                                                             KSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                         PVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELNITAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCPPYI- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Saito N., Arakawa K., Suzuki T., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chicken VIP receptor cDNA, tissue distribution
                                                                                                                             |:||:||||::|:||
FMSFILRATAVFIKDM------ALFNNGETDHCSEAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 780.5; DB 13; Length
Pred. No. 5.3e-57;
76; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ization.";
to the EMBL/GenBank/DDBJ databases
164.1; -.
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8191 MW; 7AE4796ADCB08FF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 15, Last sequence update)
1. 16, Last annotation update)
PEPTIDE RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSECRETIN.
PROTEIN_RECEP_F2_1; 1.
PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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296 VARATLADARCWELSAG-DIKWIYQAPILAALGLNFILFLNTVRVLATKIWETNAVGHDT 354 | 110 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 CKTAVTEPOFCILTNYEWILLVEGLYLQTILTLTPVSORKYFWWYILLIGWGVPSVVLIVWV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 CKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAANA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMODDPQNSIEATSVDKSQYIG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 QSQJGCWTDWDGIRCWQTAKTGQLINVSCSDVFQHISNTQGFIYRNCSSNG-W----- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 NKTWANYSDCLRFLOPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 QEGEGNCFPEWDGLICWPRGTVGKISAVPCPP-YIYDFNHKGVAFRHCNPNGTWDFMHSL 115
                                                                                                                                                                                                                                                                          388 VAVLYCELNGEVQSEIKRKWRSWTVNRYFAVDLKQQRHPSLASGGVNGGTQLSILSKSSS 447
                                                                                                                                                                                                                                        409 VSIIYCYCNGEVQAEVKKMWSRWNL----SVDWK--RTPPCGSRRC-GSVLTTVTHSTSS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              073768;
073768;
073768;
071-808. (TrEMBLrel. 07, Last sequence update)
01-806.1998 (TrEMBLrel. 16, Last annotation update)
01-806.1998 (TrEMBLrel. 16, Last annotation update)
01-807.1998 (TrEMBLrel. 16, Last annotation update)
01-807.1998 (TrEMBLrel. 16, Last annotation RECEPTOR.
01-807.1998 (Goldfish)
Carassius auratus (Goldfish)
Carassius auratus (Goldfish)
Carassius (Metarotata)
Actinopterygii; Teleostei; Euteleostei; Ostariophysi:
Cyprinformes; Cyprinidae; Cyprininae; Carassius.
                                                                                                                                                                     349 AVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFF 408
                                                                                                                                                                                           Length 438;
                                  230 KSQYIGCKIAVVMFIYELATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAA
171 RKLHCTRNFIHMNLFVSFMLRAISVFIKDGVLXA------EEDSDHCFVHT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       личо; пил.п., т. МИ; СЗ516А52D692C339 СRC64;
438 AA; 50305 МИ; СЗ516А52D692C339 СRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.2%; Score 702.5; DB 13; Query Match Similarity 35.5%; Pred. No. 1.7e-50; Best Local Similarity 35.5%; Pred. No. 1.74.7; Matches 148; Conservative 81; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF000249; 7Em_2: 1.
Pfam: PF000249; GPCRSECRETIN.
PRINTS: PR00249; G_PROTEIN_RECEP_F2_2; UNKNOWN_1.
PROSITE: PS00650; G_PROTEIN_RECEP_F2_2; UNKNOWN_1.
SMART: SM0008; HOTHER: 1. C3516A52D692C339 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Rivier J., Chow B.K.C.; Chan K.W., Yu K.L., Rivier J., Chow B.K.C.; Chan K.W., Yu K.L., Rivier J., Chow B.K.C.; Neuroendocrinology 0:0-0(1998).

Neuroendocrinology 0:0-0(1998).

EMBL: AFO48819; AAC15698.1; ---

InterPro; IPR001879; ---

InterPro; IPR001879; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA.
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                                                                                                                                                                                                                                                                                                                                                   QSQVAAAHAWCLSLAKLP 479
                                                                                                                                                                                                                                                                                                                                                                                     448 OIRMSSPLAETVNL-NLP 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 SLNKTWANYSD-CL---RELOPDISIGKOEFCERLXVMYTVGYSISFGSLAVAILIIGYF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGEGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDF----NHKGVAFRHCNPNGTWDFMH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 DGKFECPWEWDNLTCWEATSVGKVVEVNCPE-LEDEMSPEEGPGKISRNCTEFG-W---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 GLGWEIRMHCELFFNSFOGFFVSIIYCKCNGEYOAEVKKMWSRWN----LSVDWK-RTPP 442
                                                                                                                                                                                                                                                                                                                                                                                                 Carassius auratus (Goldfish). Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Euteleostei; Ostariophysi; Ratinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Carassius. NCBL_TaxID-7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-ANG-1998 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation POLYPEPTIDE TYPE 1 RECEPTOR
PITULIARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE 1
                                                                                                                                                                                                                                                                                                                              208 FFSERKYEWWYILIGWGAPSVFITAWTVVRIYFFNVGCWEEIIETPIWWIIKTPILVSIL 267
                                                                                                                                                                                                                                                                                                                                                                             328 LNFILFLNTVRVLATKIWETNAVGHDTRKOXRKLAKSTLVLVLVFGVHYIVFVCLPHSFT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                        269 FFSDTKYLWGFILLIGWGFPAAFVAAWAVARATLADARCW-ELSAGDIKWIYQAPILAAIG 327
                                                                                                                                                                                                                                    209 ELESLIMODDPONSIEATSVDKSOYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVA 268
                                                                                                                                                                                                                                                        149 TVGYSISFGSLAVAILIIGYFFRLHCTRNYIHMHLFVSFMLRATSIFVKDRVYHAHIGVK 208
                                                                                                                                                                                   54 FLTTFLGNVSRNCTSOGWTDVYPAPYAVACGYDS-----NSTPGEEGTAFYGTVKTGY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. M.Y., Shea W.L.C., Chang J.P., Chow B.K.C.; Wong A.O.L., Leung M.Y., Shea W.L.C., Chang J.P., Chow B.K.C.; Submitted (FBE-1998) to the EMBL/GenBank/DDBJ databases. BMBL; AF048820; AAC15699.1; "...InterPro; IPR000832; "...InterPro; IPR001879; "...InterPro; IPR01879; "...
                                                                                            YDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQE--FCERLYVMY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.5%; Score 713; DB 13; Length 465; Pred. No. 2.5e-51; Indels 54; Conservative 90; Mismatches 138; Indels 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53459 MW; 9779A95EDBFD1DC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFam; PF00002; 7tm_2; 1. PRINTS: PR00249; GPCRSECRIN.RECEP_F2_1; 1. PROSITE: PS00649; G_PROTEIN_RECEP_F2_2; 1. PROSITE: PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 CGS-----RRCGS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 SGSNGTNFSTQISMLTKCSPKTRRCSS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00008; HormR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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073769
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NAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGF 407
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                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PITUITARY GROWTH HORMONE-RELEASING HORMONE RECEPTOR
                                                                                                                                                                                                                                   423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲:
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PRINTS; PR00249; GPRCRECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1;
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2;
                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.99
Matches 149; Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000832; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00008; HormR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001879; -
                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                          | ::::: :|
452 QIRMSSINA 460
                                                                                                                          462 OSQVAAAHA 470
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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                                                                                                                                                                                                                                   09N1F8
 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 FRRLHCTRNYIHMHLEVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFVAAWAVARATLADARCWELSAG-DIKWIYQAPILAAIGLNFILFLNTVRVLATKIWET 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 ICVTIMAVLRLHFDNLGCWDTNNNTGLWWVIKGPVIGSIMINFVLFVGIIILLVQKL-QS 334
                 355 RKQYRKLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYC 414
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLLLGFWASQVASMHPYCIIKKEEEACL---EKIQRYEIEMWNDTQSG---CPGMWDNIT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 WLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQ-CELNITAQLQEGEGCCFPEWDGLI 71
                                                                                                                                                                                                                  YCNGEVQAEVK-KMWSRWNLSVDWK-RTPPCGSRRCGSVLTTVTHSTSSQSQVAAAH 469
                                                                                            385 FLNGDVQAELKRRLWT------WQTQTHLSPSKKRQVTVTQIMMHDSSHSQTAVSN 434
                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                             Hu Z., Lelievre V., Chao A., Zhou X., Waschek J.A.;
"Characterization and mRNA distribution of a cloned pituitary
adenylate cyclase-activating polypeptide type I receptor in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 685.5; DB 13; Length
Pred. No. 4.9e-49;
7; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53424 MW; D16C413523EFAE43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00002; 7tm_2; 1.
PRINTS; PR00249; GPCRSECRETIN.
PRODOM; PD000094; -; 2.
PROSTTE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                       465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinology 0:0-0(2000).
EMBL; AF187878; AAF16939.1;
InterPro; IPR000832; -.
InterPro; IPR001781; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00008; HormR; 1.
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001879; -.
                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus brain.
                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                        09PTK1;
                                                                                                                                                                                      Q9PTK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                         461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 MPNSTLGCPRIWDGLLCWPTAGSGEWVSLPCPAFFSHFSSEPGAVKRDCTIAG-W----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 LNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 TRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 PRNYIHTQLFITFILKAAAVFLKD-------ATLFHQENTDHCSFST-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 AVARATLADARCWEL-SAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VWGACVL--CLL-----GPLPI-----VLGHVHPECDVITQLREDEQACLQAAEG
                                                         408 FVSIIYCYCNGEVQAEVKKMWSRWNL----SVDWKRTPP--CGSRRCGSVLTTVTHSTSS
                                                                                       335 PDIGGNESSIYLRLARSTLLLIPLFGIHYTVFAFSPEN---VSKRERLVFELGLGSFQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Connor E.E., Ashwell M.S., Dahl G.E.;

Connor E.E., Ashwell M.S., Dahl G.E.;

"Sequencing and expression of bovine pituitary growth hormone-
releasing hormone receptor mRNA.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF184896; AAF63099.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 636; DB 6; Length 423
Pred. No. 5.8e-45;
By Mismatches 163; Indels
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                                                                                                                                                                                                                                                                                                                             SECTENCE FROM N.A.
Takata M., Tarumi O., Watanabe S., Sekikawa K.;
"Molecular cloning of bovine growth hormone-releasing hormone receptor
    413
                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------WDGLICWPRGTVGKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAW 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVARATLADARCWEL-SAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                          Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
354 TRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIY
           CYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTH---STSSQSQVAAAHA
                                                     5 WGACVL--CLL------GPLPI------VLGHVHPECDVITQLREDEQACLQAAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 TRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VWGWLMLGSCLLARRQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNCFPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.8%; Score 633; DB 6; Length 44 31.7%; Pred. No. 1.1e-44; Live 84; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022597; BAA84960.1; -.
InterPro; IPR001893; -.
InterPro; IPR001879; -.
Pfam; PF00002; 7tm_2; 1.
PROMIS: PR00249; GPCRESCRETIN.
PROSITE; PS00649; G_PROTEIN.RECEP_F2_1; 1.
PROSITE; PS00659; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                 Masuhiro T., Tarumi O., Watanabe S., Sekikawa K.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 AA; 49251 MW; B8E11893EFC3EBB8 CRC64;
                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
GROWTH HORMONE-RELEASING HORMONE RECEPTOR LONG FORM
                                                                                                                                                              441 AA.
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.7%
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00008; HormR; 1.
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  NCBI_TaxID-9913;
                                                                                                        423
                                                                                    WC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
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                                                                                                        422 AC
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                                          414
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13;
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Takata M., Tarumi O., Watanabe S., Sekikawa K.;
"Molecular cloning of bovine growth hormone-releasing hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEPFPPYPEACP-VPLELLTEEKSYFSAVRIIYTMGHSVSAAALLVAIIILVALRRLHC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 VGCKLAFEDVACWDLDDSSPYWWIIKGPIVLSVGVNFGLFLNIIRILLRKLEPTQGSLH- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------WDGLICWPRGTVGKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAW 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVARATLADARCWEL-SAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VWGACVL--CLL------GPLPI-------VLGHVHPECDVITQLREDEQACLQAAEG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
263 VGCKLAFEDVACWDLDDSSPYWWIIKGPIVLSVGVNFGLFLNIIRILLRKLEPTQGSLH-
                                                                                                   TRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 MPNSTLGCPRIWDGLLCWPTAGSGEWVSLPCPAFFSHFSSEPGAVKRDCTIAG-W----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022596; BAA84959.1; -.
InterPro; IPROU892; -.
InterPro; IPROU8799; -.
Pfam; PF00002; 7tm_2; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GROWTH HORMONE-RELEASING HORMONE RECEPTOR SHORT FORM
                                                                                                                                                                      414 CYCNGEVQAEVKKMWSRWNLS-----VDWKRTPPCGSR 446
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
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Matches 139; Conserv
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Search completed: September 21, 2001, 17:09:25 Job time: 198 sec



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APPLICANT: Soppet, Daniel R
APPLICANT: Y1, Li
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 28
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100.0%; Pred. No. 2.5e-294;
ive 0; Mismatches 0;
          US-08-855-213-17
US-08-811-897A-22
US-08-811-897A-20
US-08-811-897A-21
US-08-811-897A-21
US-08-855-213-21
US-08-811-897A-27
US-08-811-897A-27
US-08-811-897A-25
US-08-811-897A-25
US-08-811-897A-25
US-08-811-897A-14
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3-08-811-897A-29
3-08-855-213-29
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US-08-855-213-15
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N: 435
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: THE PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bain,
                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08468011A Patent No. 6030804
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Carella, Byrne, Ba
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION
TELEPHONE: 201-994-1700
TELEFAX: 201-994-174
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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; MOLECULE TYPE: protein
US-08-468-011A-2
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Matches 54
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Sequence 21,
Sequence 5, P
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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          version 4.5
- 2000 Compugen Ltd.
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PCT-US95-07085-2
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US-08-142-551B-125
US-08-468-249A-19
US-08-468-249A-21
US-08-468-249A-21
US-08-468-249A-21
US-08-142-439A-5
US-08-142-439A-5
US-08-11-897A-5
US-08-13-816A-9
US-08-538-816A-9
US-08-538-816A-19
US-08-538-816A-19
US-08-538-816A-19
US-08-538-816A-19
US-08-813-818A-19
US-08-813-818A-19
US-08-855-213-18
US-08-855-213-18
US-08-811-897A-18
US-08-811-897A-23
US-08-811-897A-23
US-08-811-897A-23
US-08-811-897A-23
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Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw mode]
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          GenCore
Copyright (c) 1993
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                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
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2907
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Perfect score:
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NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH
                                                                                                                                         MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
                                                                                                                                                       VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT
                                                                                                                                                                                                         241 VMFIXFLATNYXWILVEGLYLHNLJFVAFFSDTKYLMGFILLIGWGFPAAFVAARAT
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                                      GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA
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E: Stewart & Olstein
6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-393
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US95/07085
05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07068-1739
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9507085 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Soppet, Daniel R
APPLICANT: Y1, L1
APPLICANT: Roben, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Pa
TITLE OF INVENTION: G-Protein Pa
CORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 05-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Roseland
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 6
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                                                                                                                                                                               Length
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ADDRESSEE: NO. 56703600 NO. 5670360disk of NO.
                                                                                                                                                                             100.0%; Score 2907; DB 5;
100.0%; Pred. No. 2.5e-294;
iive 0; Mismatches 0;
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Patent No. 5670360
PERRAL INFORMATION:
APPLICANT: Thoren, Bernard
TITLE OF INVENTION: Receptor for th
TITLE OF INVENTION: (GLP-1)
               TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
201-994-1700
                                                                                                                                                                                                               Matches 541; Conservative
                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07085-2
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                                                                                                                                                                                              Similarity
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TELEPHONE:
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US-08-142-439A-6
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SSEE: No. 58467470 No. 5846747disk of No. 5846747th America, Inc. 1405 Lexington Avenue, Suite 6400
New York
       494 VSHTSVTNVGPRGGLALSLS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLPSSGPE 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :|:| || ||||:|: |: || || || 24 ALVDADDDVITKEEQIILLENAQAQCEQRLKEVLRVPELAESAKDWMSRSAKTKKEKPAEK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                          for the Glucagon-Like-Peptide-1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Score 1397; DB 2;
48.0%; Pred. No. 6.4e-137;
ilve 94; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439
FILING DATE: 24-NOV-93
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATORREY/AGENT INFORMATION:
NAME: HAITINGTON, James J.
                                                                         551 PGTKDDGYLNGSGLYEPMVGEOPPPLLEEERET
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                                                                                                                                                                    Sequence 6, Application US/08869477
Patent No. 5846747
                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 101/4-020.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~weitter: IBM PC Compatible
~~noitter: IBM PC Compatible
                                                                                                                                                                                                                       Bernard
Receptor f
(GLP-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 48.1%
Best Local Similarity 48.0%
Matches 275; Conservative
                                                                                                                                                                                                                   APPLICANT: Thorens, Ber
TITLE OF INVENTION: REC
TITLE OF INVENTION: (GL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                               STREET: 405 Lexir
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
                                                                                                                                                                                                          GENERAL INFORMATION:
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TOPOLOGY: lir
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                               US-08-869-477-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA 341
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; DB 1;
6.4e-137;
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48.0%; Pred. No. 6.4e-
tive 94; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AQLDSDGTITIEEQIVLVLKAKVQCELNIT-----
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24 NOV-93
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Didelphis virginiana
                                                                                                                                                                                                                                                                        NAME: Harrington, James J. REGISTRATION NUMBER: 38,711 REFERENCE/DOCKET NUMBER: 37: TELECOMMUNICATION INFORMATION: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                        TELEFANCE. 22.867 0298
TELEFAX: 212.867 0298
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 585 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 48.0975; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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ORGANISM: Dic
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Best Local Simi
Matches 275;
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                                                                                                                              102 HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV 161
                                                                                  342 TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELE 400
                                                                                                                                                                                                                                                                                                                                  FNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTH--- 457
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                                                                                                                                                                                                                                                                                                                                                                                                 -STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED
                 APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 SGRQRDDILM-----EKPSRPMESNPDT 539
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APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/965,677
FILING DATE: 22-CCT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000
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321 FGWGLPAVFVAVWTVRATLANTECMDLSSGNKKWIIQVPILAAIVVNFILFINIIRVLA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV 161
                                                                                                                                                                                                                                                                                                                                                                                                     494 VSHTSVINVGPRGGLALSLS--PRLAPGAGASANGHHOLPGYVKHGSISEN-SLPSSGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 -STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED
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                                                                                                                                                                                                                                                                                                      Length 585;
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TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                47.9%; Score 1392; DB 2;
47.8%; Pred. No. 2.1e-136;
tive 92; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                24 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE----
                                                                                                                                                                                                                       /note= "PTH receptor"
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225 Franklin Street
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TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 125
SEQUENCE CHARACTERISTICS:
                                                                              585 amino acids
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.84
Matches 274; Conservative
                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                           NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION:
US-08-142-551B-125
                                                                                                                        unknown
                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
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                                                                                                                      TOPOLOGY:
                                                                              LENGIH:
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                                                                                                                                                             FEATURE:
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47.7%; Score 1388; DB 2; 54.6%; Pred. No. 4.5e-136; tive 73; Mismatches 92;
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                                          | : | : | : | : | 551 PGTKDDGYLNGSGLYEPMVGEQPPPLLEEERET
   517 SGRQRDDILM-----EKPSRPMESNPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Sequence 18, Application US/08468249A Patent No. 5886148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 54.69
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-468-249A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 FNSFQGFFVAIIYCFCNGEVQAEIKKSWSRWTLALDFKRKARSGS-----STYSYGPM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -STSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKED 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 VSHTSVTNVGPRGGLALSLS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLPSSGPE 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 HCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAV 161
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                                                                                                                     COMPUTER: FALOHY GENERAL COMPUTER: FALOHY GENERAL COMPUTER: TABM PC COMPUTER: TABM P
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47.8%; Pred. No. 2.1e-136;
tive 92; Mismatches 137;
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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RY: USA
02110-2804
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4 LYPQAEESREVSDRSRLQDGFCLPEWDNIVCWPAGVPGKVVAVPCPDYFYDFNHKGRAYR 143
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GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE TO STATEM.

SOFTWARE TO STATEM.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A

FILING DATE: 06-JUN 1995

CLASSIFICATION 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475

FILING DATE: 06-APR 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702

FILING DATE: 04-MAY-1991

ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-08-468-249A-21
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222 SIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFIL 281
                                                                                 321 FGWGLPAVFVAVWVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILFINIIRVLA 380
                                                                                                                                  342 TKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400
                                                                                                                                                   Gaps
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                   FIEPPPADKAGFVGCRVAVIVFLYFLTINYYWILVEGLYLHSLIFMAFFSEKKYLWGFTL
                                                                282 IGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87;
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA TITLE OF INVENTION: ENCODING SAME NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                    FNSFQGFFVSIIYCYCNGEVQAEVKKMMSRWNLSVDWKRTPPCGS 445
                                                                                                                                                                                                                   SOFTWARE: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.8%; Score 1331.5; DB 2;
46.6%; Pred. No. 4.3e-130;
tive 86; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00786/071003
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APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08468249A Patent No. 5886148 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTR: USA
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP C COMPATIBLE
COMPUTER: INP C COMPATIBLE
COMPUTER: INP C COMPATIBLE
COMPUTER: INP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET UNMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISIES:
LENGTH: 591 amino acids
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amino acid
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Matches 270; Conserva
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US-08-468-249A-20
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                                261
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157 GSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESL--- 213
                                                                                                                                                                                                                                                                                                                                                                                                          270 FSDTKYLWGFILLIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN 329
                                                                                                                                                                                                                                                                                                                                                                                                                                      GVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISF
                                                                                                                                                                                                                     200 ASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTLDEAERLTEE
                                                                                                                                                                                                                                                                                                 214 ----IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAF
                                                                                                                                                                                                                                                                                                                              260 ELHIIAQVPPPPAAAAVG----YAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAF
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Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 ETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQE 585
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                                                                                                                                                                                                                                                                                                                                                         269
                                                                                                                                                                                                                                                                                         GVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISF 156
                                                                                                                                                                                                                                                                                                       GSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESL--- 213
                                                                                                                                                                                                                                                                                                                                                                                                         FILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS-FTG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 LGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 SYGPMVSHTSVTNVGPRVGLG------LPLSPRLLPTATTNGHPQLPGHAKPGTPAL 545
                                                                                                                                                            Gaps
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                                                                                                                                                                                                   58 -----EGEGN------CFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHK
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                                                                                                                                                            91;
                                                                                                                                  Length 593;
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                                                                                                                                                            Indels
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                                                                                                                                45.8%; Score 1331.5; DB 2
47.4%; Pred. No. 4.3e-130;
tive 80; Mismatches 135;
                                                                                                                                                                                   22 ARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQ-
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APPLICANT: Thorens, Bernard TITLE OF INVENTION: Receptor for TITLE OF INVENTION: (GLP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
                                                                                                                                Query Match
Best Local Similarity 47.44
Matches 276; Conservative
                                                                              MOLECULE TYPE: protein US-08-468-249A-21
                                                                   linear
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                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WAVARATLADARCWELSA-GDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 --WDGLICWPRGTVGKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHSLNKTWANYS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.6%; Score 801; DB 1; Length 44 37.3%; Pred. No. 5.4e-75; ive 81; Mismatches 149; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: HATLINGTON, James J.
REGISTRATION NUMBER: 38,711
                                                                                                                                                                                                                                                                                                                                                                                                              3756.204-US
                                                                                               APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 449 amino acids TYPE: amino acid
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) STRAIN: Sprague-Dawley
US-08-142-439A-5
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Best Local Similarity
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TOPOLOGY: lir
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213 VGCKLVMIFFQYCIMANYAWLLVEGLYLHTLAISFFSERKYLQAFVLLGWGSPAIFVAL 272
                                                                                                                66 KMWDNLTCWPATPRGQVVVLACPLIFKLFSPTQGLNVSRNCTDEG------WTP- 113
                                                                                        WAVARATLADARCWELSA-GDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGH 352
                                                                                                                                                                                               333 ET-NHYKRLAKSTLLIIPLFGIHYIVFAFSPED----AMEVQLFFELALGSFQGLVVAVL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 PEWDGLICWPRGTVGKISAVPCPPYIYDFN-HKGV-AFRHCNPNGTWDFMHSLNKTWANY 122
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        IGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAA
                                                                                                                                                                              DTRKQYRKLAKSTLVLVLVFGVHXIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSII
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                                                                                                                                                                                                                                                                                   413 YCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQ 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hsiung, Hansen M.
APPLICANT: Smith, Dennis P.
APPLICANT: Zhaft, Xing-Yue
APPLICANT: Zhaft, Xing-Yue
TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 785; DB 1; Length 458;
Pred. No. 2.6e-73;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh IIci compatible
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word for Macintosh v.5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,817C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08112817C Patent No. 5573928
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37.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Richard B.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 458 amino acids
amino acid
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Best Local Similarity 37.09
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-112-817C-2
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                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58467470 No. 5846747disk of No. 5846747th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 --WDGLICWPRGTVGKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHSLNKTWANYS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 GLWDNMSCWPSSAPARTVEVQCPKFLLMLSNKNGSLFRNCTQDG-------WSE-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 DCLRFLQPDISIG---KQEFCER-----LYVMYTVGYSISFGSLAVAILIIGYFRRLH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ---TFPRPDLACGVNINNSFNERRHAYLLKKVMYTVGYSSSLAMLLVALSILCSFRRLH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 CTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQL-QEGEGNCFPE----- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LLLRLLLLTKAA----HTVGVPPRLCDVRRVLLEERAHCLQQLSKEKKGALGPETASGCE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                             APPLICANT: Thorens, Bernard
IIILE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 2; Length 449;
5.4e-75;
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFENCE/DOCKET NUMBER: 3756.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.6%; Score 801; 37.3%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439
FILING DATE: 24-NOV-93
APPLICATION NUMBER: DK 398/92
PILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/869,477
                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
Sequence 5, Application US/08869477 Patent No. 5846747
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.39
Matches 176; Conservative
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TELEPHONE: 212 867 0298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
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US-08-869-477-5
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SDCLRFLQP-----DISIGKQE----FCERLYVMYTVGYSISFGSLAVALLIIGY 168
                                                             FRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSV 228
                                                                                                                        DKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILLIGWGFPA 288
                                                                                                                                        10 SKGS-VGCKAAVVLFQYCVMANFFWLLVBGLYLHTLLAVSFFSERKYFWGYIFVGWGVPS 268
                                                                                                                                                                                    289 AFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETN 348
                                                                                                                                                                                                      349 AVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFF 408
                                                                                                                                                                                                                                                                                                                               -----LEPGPYPIACGMDDKASGLDEQQTVFYNSVKTGYTIGYSLSLAALLVATAILSL 167
                                                                                                                                                                                                                                                                 409 VSIIYCYCNGEVQAEVKKMWSRWN----LSVDWKRTPPCGSRR---CG---SVLTTVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHIMAMOTO, NO. 5858/78710
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
TITLE OF INVENTION: 5410 PROTEIN, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,897A
FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 44168-DIV TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56, Application US/08811897A Patent No. 5858787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: February 25, 1994
ATTORNEY/AGENT INFORMATION:
ATHORNER RESIDENT DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KITADA, Chieko
ISHIBASHI, Yoshihiro
HOSOYA, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/202,986
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MIYAMOTO, Yasunori
HABATA, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHTAKI, Tetsuya
MASUDA, Yasushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617)523-3400
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONDA, Haruo
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US
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         457 -- HSTSSQSQVA 466
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STREET: 100
-mv: Boston
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STATE: M
COUNTRY:
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APPLICANT:
APPLICANT:
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APPLICANT: Mojsov, Svetlana
APPLICANT: Wei, Yang
TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                         137 --KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWE-LSAGD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373
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                                                                                                                                                                                                                                                                                                        EYLOLIEIQRQQCLEE--AQLENETTGCSKMWDNLTCWPTTPRGQAVVLDCPLIFQLFAP 97
                                                                                                                                                                                                                                                                                                                                                90 IYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQP---DISIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 IKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKOYRKLAKSTLVLVLVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQFFFVSIIXCYCNGEVQAEVKKMWSRWNL
                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S--VDW--KRTPPCGSRR---CG---SVLTTVT----HSTSSQSQVAAA-HA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1324;
                                                                                                                                                                                                                                                                36 EQIVLVLKAKVQCELNITAQLQEGEGNCFPEWDGLICWPRGTVGKISAVPCP
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                   Query Match 26.6%; Score 773; DB 2; Lk Best Local Similarity 36.9%; Pred. No. 2.3e-71; Matches 174; Conservative 78; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/538,816A FILING DATE: 03-OCTOBER-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08538816A Patent No. 5831051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 amino acids
                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack CITY: Hackensack STATE: New Jersey COUNTRY: USA 7TP: 07601
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                      ; TOPOLOGY:
US-08-811-897A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-538-816A-2
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RECEPTOR FOR PEPTIDE HORMONES INVOLVED
IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 PCPPYIYDF-NHKGVAFRHCNPNGTWDFMHSLNKTWANYSDCLRFLQPDISIGKQEFCER 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 LYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFVKDRVVHA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 VLVLKAKVQCELNITAQLQEGEGNCFP-------EWDGLICWPRGTVGKISAV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 HIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIK-WIYQAPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                  Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.5%; Score 713.5; DB 2 33.6%; Pred. No. 6.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600-1-136 CIP
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/538,816
FILING DATE: 03-OCTOBER-1995
APPLICATION UNDRER: US 08/437,466
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/076,651
                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
DESCRIPTION: RPACAP-3/RVIP-2
                                                                                                Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 437 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LECURES 201 TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                  CORRESPONDENCE ADDRESS:
         TITLE OF INVENTION: R
TITLE OF INVENTION: I
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                      New Jersey
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                                                                                                            STREET: 411 ...
CTTY: Hackensack
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24.5%; Score 713.5; DB 2;
Best Local Similarity 33.6%; Pred. No. 6.8e-66;
Matches 163; Conservative 87; Mismatches 156;
                                                                          CLASSIFICATION: 536
TATORNEY FAGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-136 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/437,466
FILING DATE: 09-MAY-1995
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Sequence 2, Application US/09076651

Patent No. 5882899

GENERAL INFORMATION: APPLICANT: MOJSOV, SVETIANA
APPLICANT: Wei, Yang
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TOPPOLGY: linear
MOLECULE TYPE: protein
RPACAP-3/RVIP-2
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: single
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	Db 34	347 PIGISSTYQILFELCVGSFQGLVVAVLYCFLNSEVQCELKRRWR 390	0
•	Oy 44	443 CGSRRCGSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSR 502	2
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_	Db 43	430 LQSET 434	
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Human tethered Human tethered

Human PTRR seven t Human kidney PTH/P PTH/PTHTP receptor PTH/PTHTP extracel Parathyroid hormon Human VIPR seven t

Parathyroid

Human

Opossum parathyroi Zebrafish PTH3R re Zebrafish parathyr PTH/PTHrP intracel

Human GR C-termina Human qlucagon-lik glucagon rec GLR seven tr Rat glucagon-like Human glucagon-lik

Human Нитап

Human glucose-depe Human GIP receptor Human GIP receptor

Human GIPR seven t

Porcine vasoactive VIP receptor prote

Title: Perfect score: Sequence:

OM protein

Run

Scoring table:

Minimum DB Maximum DB

Database

Word size Searched:

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calcium; signal transduction; agonist; antagonist; hypocalcaemia; hyperphosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephroliasis; therapy; diagnosis.
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         AAR30187
AAY96985
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AAB71878
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 95WO-US07085
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 AAW12695;
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 RESULT
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Million cell updates/sec
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Opossum kidney PTH
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                                                                  Search time 22.32 Seconds
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// SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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        4.5
Compugen Ltd
                                                                            (without a 1469.426 )
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         GenCore version
Copyright (c) 1993 - 2000

    protein search, using sw model

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Result Š.

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vascular; hepatic; antiasthma; anitmicrobial; antiinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoimmunity;
                                                                                                       Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory;
                                                                         Human PTR2 seven transmembrane domain.
                                                                                                                                                                               graft rejection; cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                            29-FEB-2000; 2000US-0515781.
                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000WO-US21278
                                            03-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-138653/14
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                                                                                                                              A novel 7-transmembrane receptor (AAW12695) has been identified as a human G-protein parathyroid hormone (PTH) receptor, designated HLTDG74. It shows 48.2% homology to the human PTH receptor. Its amino acid sequence was deduced from a cDNA clone (AAT56619) isolated from a human T cell lymphoma tissue cDNA library. Recombinant HLTDG74 can be produced in transformed host cells and used to screen for (ant)agonist cpds. Agonists may be used to prevent or treat e.g. hypocalcaemia, hypophosphatemia, hypoparathyroidism and chronic tetany by stimulating an increase in serum calcium levels. Anteagonists can be used to inhibit the receptor e.g. for the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism, hypophosphateamia, kidney stone, nephroliasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMFIYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAKSTLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAEVKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKEDSGRQRDDILMEKPSRPMESNPDTE
                                                          ıuentiiy (ant)agonists, used in the treatment of hypo- or
hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
                                              t
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0
                                                                                                                                                                                                                                                                                                                                                                         Length 541;
                                              HLTDG74 - used
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 541; DB 18; Best Local Similarity 100.0%; Pred. No. 0; Matches 541; Conservative 0; Mismatches 0;
                                         Human G-protein parathyroid hormone receptor, identify (ant)agonists, used in the treatment
                                                                                                  Claim 9; Fig 1A-E; 62pp; English.
WPI; 1997-043068/04.
N-PSDB; AAT59619.
                                                                                                                                                                                                                                                                                                                              541 AA;
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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h1571. h1571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory diseases including sthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies may be used to down requiate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR may be.
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Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 lgaslhvwgwlmlgscllaraqldsdgtitieeqivlvlkakvqcelnitaqlqegegnc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 363; Pred. No. 0;
                                                                                                                           Disclosure; Fig 2; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.18;
99.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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RESULT 2 AAB71875 ID AAB71875 standard; Protein; 550 AA.

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AAB80559 standard; Protein; 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anorectic, neuroleptic, antideperssion, nootropic, analgesic, antimizatine, antidiabetic, osteopathic, hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective activities, and is an PTH receptor antegonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor and person and a part of the presence of a disorder mediated by binding a person of the PTH2 or pTH1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                   Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand; parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic; PTH2 receptor binding activity; antidepression; neuroleptic; analgesic; antimigraine; antidiabetic; osteopathic; hypertensive; cardiant; cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist; obesity; eating disorder; metabolic disorder; mental disorder; headache; schizophrenia, dementia; acute pain; chronic pain; migraine; headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism; hypertension; conqestive heart failure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis;
                                                                                                                                                                     FVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMF 243
                                                                ARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAK 363
                                                                                                                                                      STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other
             IYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New parathyroid hormone type 2 or 1 receptor ligand, useful for treating e.g. migraine or headaches, hypertension, obesity and ot eating or metabolic disorders, mental disorders and osteoporosis
                                                                                                                                                                                                        Human PTH2 receptor amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                    AA.
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                                                                                                                                                                                                                                                                                                 AAB80560 standard; Protein; 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2000; 2000WO-US16776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139335
                                                                                                                                                                                                                                                                                                                                                     26-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usdin TB, Hoare SRJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-122833/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200077042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukodystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                           AAB80560;
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184
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                                                                                                                                                                                                                                                                                    AAB80560
                                                                                                                                                                                                                                                                          RESULT
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schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. The present sequence represents a PTH2 receptor which is used in the exemplification of the present invention.
depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLAD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAE 423
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                      4 Igaslhvwgwlmlgscllaraqldsdgtitieeqivlvlkakvqcelnitaqlqegegnc 63
                                                                                                                                                                                                                                                                                                                                                                                               4 LGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIHMHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMF
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                    Score 262; DB 22; Length 550;
Pred. No. 1e-259;
                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAA
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                               48.4%;
                                                                                                                                                                                                                                                                                                                                                 462; Conservative
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                               550 AA;
                                                                                                                                                                                                                                  Sequence
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Best Local S
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Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand; parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic; PTH2 receptor binding activity; antidepression; neuroleptic; analgesic; antimigraine; antidiabetic; osteopathic; hypertensive; cardiant; cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist; obesity; eating disorder; metabolic disorder; mental disorder; depression; schizophrenia; dementia; acute pain; chronic pain; migraine; headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism; hypertension; congestive heart failure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis; Rat PTH2 receptor amino acid sequence. (first entry) Leukodystrophy

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92US-0864475.
                                                                                                                                                                                                                                                                                                                                515 AA;
                                                                                        N-PSDB; AAQ29604
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                                               Abou-samra A,
 06-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1991;
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Schipani E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR92275;
                                                         Segre GV;
                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                   The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anoretic, neuroleptic, antidepression, nootcopic, analgesic, antimitarine, antidiabetic, osteopathic, hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders; osteoporosis,
                                                                                                                                                                                                                                                                                                                                                            hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. The present sequence represents a PTHZ receptor which is used in the exemplification of the present invention.
                                                                                                                                                                    New parathyroid hormone type 2 or 1 receptor ligand, useful for treating e.g. migraine or headaches, hypertension, obesity and other eating or metabolic disorders, mental disorders and osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parathyroid hormone; related protein; calcium; antagonist; antibodies; hypercalcaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Opossum kidney PTH/PTHrP receptor prepd. from clone OK-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 38; DB 22; 100.0%; Pred. No. 3.2e-30; 1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 WIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR27704 standard; Protein; 515 AA
                                                                                                                                                                                                                 Example 4; Fig I; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0.,
100.0%; Pre
                                                       L5-JUN-2000; 2000WO-US16776
                                                                             99US-0139335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                         Hoare SRJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Didelphis virginiana.
                                                                                                                                               WPI; 2001-122833/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             546 AA;
           WO200077042-A2
                                                                             15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1992;
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                                  21-DEC-2000
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                                                                                                                          Usdin TB,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Matches
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The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP) receptor protein sequence was deduced form the DNA sequence of the clone OK-H, isolated from opossum kidney (OK) cells. The protein may be used in a therapeutic compsn. to inhibit activation of PTH or PTHrP and thus reduce the level of calcium in the blood. Cpds. capable of competing with PTH or PTHRP for binding can be identified using the protein prod. and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The protein may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also AAR27705-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                             New DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis
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                                                           Schipani E;
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                                                        Kronenberg HM, Potts JT,
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(GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 gyfrrlhctrnyihmhlfvsfmlra 231
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100.0%; Pre
0; '
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91US-0681702.
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                                                     Juppner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.6
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                         and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Didelphis virginiana
                                                                                                                                            WPI; 1992-366271/44.
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Didelphis virginiana
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N-PSDB; AAQ29605.
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                               515 AA;
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                                                                              receptors (AAR92275 and AAR92776) are encoded by CDNA clones OK-H (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2 separate genes or of a laboratory artifact. The receptor induces an increase in intracellular cAMP and calcium when challenged with PTH or PTHTP. Recombinant receptors can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host cells expressing the receptor can be used for diagnostic measurement of PTH serum levels.
                                                                                                                                                                                                                                                               Gaps
                                                                         Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
          - useful for
         DNA encoding vertebrate parathyroid hormone receptor - useful diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parathyroid hormone receptor; PTH receptor; antibody; therapy; PTH-related hypercalcaemia; opossum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody to parathyroid hormone receptor - for diagnostic or therapeutic use
                                                                                                                                                                                                                                          Length 515;
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Pred. No.
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                                                                                                                                                                                                                                                                                   167 GYFRELHCTRNYIHMHLFVSFMERA 191
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                                                   Claim 1; Fig 1A-1E; 64pp; English
                                                                                                                                                                                                                                                                                                                                                             AAW73314 standard; Protein; 515
                                                                                                                                                                                                                                       Query Match
4.6%; Soc
Best Local Similarity 100.0%; Pi
Matches 25; Conservative 0;
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91US-0681702.
95US-0471494.
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06-JUN-1995;
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                               cancer etc.
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The parathyroid hormone/parathyroid hormone related protein (PTH/PTHIP)

receptor protein sequence was deduced form the DNA sequence of the
clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
is identical to the OK-H clone exept at the C-terminal tail as OK-O
encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.

The difference is attributed to a single nucleotide deleted in the OK-H
sequence causing a frame shift and an earlier stop codon. It is not
known whether OK-O and OK-H represent prods. of two separate genes or
are a laboratory artifact. The protein may be used in a therapeutic
compsn. to inhibit activation of PTH or PTHPP and thus reduce the
compsn. to inhibit activation of PTH or PTHPP and thus reduce the
or PTHPP for binding can be identified using the protein prod, and
DNAs homologous to PTH DNA can be identified using fragments of the
clone as probes. The sequence may be used for the protein of antibodies
useful for the treatment, classification, prognosis and/or treatment of
disorders related to the interaction between a cell receptor and a
ligand such as in hypercalcaemia. See also AAR27704-16.
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characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia.
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                                                                                                                                                                                                                      Length 515;
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                                                                                                                                                                                                                                                                                          0; Indels
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6.4e-17;
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                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                         207 gyfrrlhctrnyihmhlfvsfmlra 231
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                                                                                                                                                                                                                  4.6%; S
100.0%;
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Best Local Similarity 100.
Matches 25; Conservative
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us-09-236-468a-2.oli10.rag

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AAW73315;
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 RESULT 10
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AAB08188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host calls expressing the receptor can be used for diagnostic measurement of PTH serum levels.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for
                                                                                                                                                                                                  Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer; opossum.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ing vertebrate parathyroid hormone receptor - useful and treatment of e.g. hypercalcaemia, hypo-calcaemia,
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         Length 585;
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DB 13; Le.,
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7.1e-17;
        Score 25; DB
Pred. No. 7.1
0; Mismatches
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Segre GV;
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Pred. No.
                                                           207 gyfrrlhctrnyihmhlfvsfmlra 231
                                                                                                                      AAR92276 standard; Protein; 585 AA
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                                               167 GYFRRLHCTRNYIHMHLFVSFMLRA 191
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                                                                                                                                                                                 Opossum kidney PTH/PTHrP receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2A-2E; 64pp; English.
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100.0%; Pre
0;
  4.6%; Scu.
100.0%; Pre
0;
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                                                                                                                                                             (first entry)
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                             Conservative
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N-PSDB; AAT15946.
        Query Match
Best Local Similarity
Matches 25; Conserv
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Best Local Similarity
Matches 25; Conserv
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05-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer etc.
                                                                                                                                          AAR92276;
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This sequence represents the opossum parathyroid hormone (PTH) receptor OK-O, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó,
                                                                                                                                                            receptor; PTH receptor; antibody; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody to parathyroid hormone receptor – for diagnostic or
therapeutic use
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100.0%; Pred. No. 7.1e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kronenberg HM,
                                                                                                                                                                                  hypercalcaemia; opossum.
AAW73315 standard; Protein; 585 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB08188 standard; Protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 GYFRLHCTRNYIHMHLFVSFMLRA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 gyfrrlhctrnyihmhlfvsfmlra 231
                                                                                                                    Parathyroid hormone receptor OK-O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0.,
100.0%; Pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                92US-0864475.
91US-0681702.
95US-0471494.
                                                                                                                                                                                                                                                                                                                                            95US-0471494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP.
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                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Juppner |
Segre GV;
                                                                                                                                                                                                                    Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-034124/03.
                                                                                                                                                            hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV08389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                  06-APR-1992;
                                                                                                                                                                                PTH-related
                                                                                                                                                            Parathyroid
                                                                                                                                                                                                                                                           US5840853-A.
                                                                            08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                     24-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schipani E,
                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1991
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WO200109328-A1
                          08-FEB-2001
                                                                                                                                              Hodge MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR30187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR30187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                               The present sequence represents a rat secretin receptor polypeptide.
Secretin is a gastrointestinal hormone that stimulates the secretion of bicarbonate-rich pancreatic fluid. Secretin is produced by specific endocrine cells (S cells) located in the mucosa of the proximal small intestine. Secretion of secretin is stimulated by the presence of either acidic pH or fatty acids in the duodenum. The specification describes a method for modulating the growth state of pancreatic cells. The method for modulating the cells with a secretin therapeutic or product comprises contacting the cells with a secretin therapeutic or product pancreatic cells, in particular to promote the proliferation of pancreatic cells, generate functional pancreatic beta cells from pancreatic listes or cells, promote insulin production in a pancreatic siste or cells, promote insulin inhibition of secretin response in secretin-responsive cells, modify glucose metabolism in an animal to resistance, glucose intolerance or non-responsiveness, hyperglycemia, hyperinsulinemia, obesity, hyperlipidemia, hyperproteinemia or Type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; SCRC; secretin receptor; h15571; immunomodulatory; vascular; hepatic; antiasthma; anitmicrobial; antiinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoimmunity; graft rejection; cystic fibrosis.
                                                                                                                                                                                                                                    Secretin therapeutic is used to modulate the growth state of pancreatic cells to provide treatment for diabetes through modification of glucose metabolism - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%; Score 19; DB 21; Length 440; 100.0%; Pred. No. 7.8e-11; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SCRC seven transmembrane domain.
                                                                                                                                                                                                                                                                                          Disclosure; Page 88-90; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB71877 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08; P. ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 FRELHCTRNYIHMHLEVSF 187
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                                                                                                                 99US-0119575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                          (ONTO-) ONTOGENY INC
                                                                                                                                                                                             WPI; 2000-515058/46.
N-PSDB; AAA63813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 AA;
                                                                                                                                                                    Kagan D, Pang K;
                                    WO200047721-A2.
                                                                                                                 10-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                              17-AUG-2000
            Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB71877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR comparison with the seven transmembrane domain of a novel GPCR comparison with the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, hemmatological, fibrotic, hepatic and respiratory diseases including asthma, allergies (e.g. allergic and respiratory diseases), pathogenic infections, chronic inflammatory disease, organ-specific autoimmunity, arate production, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR expression and activity. The anti-GPCR antibodies and GPCR antagonists may also be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR.
                                                                                                                                                                                                                                                          Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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00.0%; Pred. No. 7.8e-11;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
/note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mature secretin receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; rat/mouse hybridoma; NG 108-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR30187 standard; Protein; 449 AA.
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.55,
100.0%; Pre-
0; '
                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 FRRLHCTRNYIHMHLFVSF 187
03-AUG-2000; 2000WO-US21278
                                                                 29-FEB-2000; 2000US-0515781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.5
Best Local Similarity 100.
Matches 19; Conservative
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/note= "r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides in samples.
                                                                                                                                                                   Lloyd C,
                                                                                                                                                                                                          WPI; 2001-138653/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 AA;
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                                                03-AUG-1999;
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99WO-US31108. 98US-0114577,

GARDELLA T KRONENBERG

Rattus sp.

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(POTT/) POTTS J T. (JUEP/) JUEPPNER H.
                                                                          WO200039278-A2
                                                                                                                                                                                                                                                                                                                        Gardella TJ,
                                                                                                                                                  30-DEC-1999;
                                                                                                                                                                                       31-DEC-1998;
                                                                                                               06-JUL-2000
                                         Synthetic.
                     Chimeric
                                                                                                                                                                                                                          GARD/)
                                                                                                                                                                                                                                          (KRON/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The secretin receptor was encoded by a DNA sequence of rat origin, contained in rat/mouse hybridoma NG108-15. The DNA sequence was obtd. from a cDNA library derived from NG108-15 cells. Expression in a suitable host allows prodn. of the receptor protein. The secretin receptor protein encoded by this gene may be used in basic research and in clinical tests, and is available in high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTH; parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; r-delta-NT/Ct; tethered receptor; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA coding for secretin receptor – is expressed in COS cells and produces a receptor protein for research and clinical use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                   'note= "potential N-glycosylation site"
                                                        'note= "potential N-glycosylation site"
                                                                                           'note= "potential N-glycosylation site"
                                                                                                                                "transmembrane domain"
                                                                                                                                                                    "transmembrane domain"
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                                                                                                                                                                                                                                                                                   "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1; 44pp; Japanese.
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Best Local Similarity 100.
Matches 19; Conservative
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374..394
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                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                'note₌
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N-PSDB; AAQ33018.
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Modified-site
                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishihara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-2000
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Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. Si sa n amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis.
                                                                                                                                                                                           linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass
                                                                                                                                                                New compound comprising an amino terminal signaling functional domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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   Jueppner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 21; 1
Pred. No. 6.2e-10;
0; Mismatches 0;
   Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 1..23
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                                                                                                                                                                                                                                                                                            Claim 22; Fig 10; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7.
100.0%; Pr.
Kronenberg HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 YFLATNYYWILVEGLYLH 262
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Matches 18; Conservative
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                                                            WPI; 2000-452384/39.
N-PSDB; AAA51734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric -
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Peptide
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Jueppner H;

Potts JT,

98US-0114577. 99WO-US31108

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New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                         Example 4; Fig 18; 119pp; English.
                                                                                                                                                                                                        Gardella TJ, Kronenberg HM,
  Chimeric - Homo sapiens.
                                                                                                                                         (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
                                                                                                                                                                                                                                  WPI; 2000-452384/39.
                                                                                                                                                                                (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                               N-PSDB; AAA51736
                                     WO200039278-A2.
                                                                                        30-DEC-1999;
                                                                                                                 31-DEC-1998;
                                                               06-JUL-2000
              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                         Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH): L is a linker molecule present n times (of parathyroid hormone (PTH): L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)): B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-TP) (1-34); R-1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening connected by inhalation unlike the large native PTH or PTH P which avoids the need for regular injections to treat osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                 New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTH; parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 21; Length 33. Pred. No. 6.4e-10;
/label- PTH-1_receptor_signal_sequence
                                                                                                                                                                                                                                                                                     Kronenberg HM, Potts JT, Jueppner H;
                                                                        /label= PTH-1_receptor
/note= "residue 182 to 480"
            24..32
/label= PTH_residues_1-9
33..36
/label= linker
37..335
/label= PTH-1_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tethered PTH-1 receptor, hdelNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96987 standard; Protein; 435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3°,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Fig 9; 119pp; English.
                                                                                                                                                                                            98US-0114577
                                                                                                                                                                  99WO-US31108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                    GARDELLA T J.
KRONENBERG H M.
                                                                                                                                                                                                                                                                                                            WPI; 2000-452384/39.
                                                                                                                                                                                                                                              (POTI/) POTIS J T. (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 AA;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA51733
                                                                                                               WO200039278-A2
                                                                                                                                                                                                                                                                                  Gardella TJ,
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                                                                                                                                                                 30-DEC-1999;
                                                                                                                                                                                           31-DEC-1998;
                                                                                                                                          06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                     Peptide
                                                                                                                                                                                                                     GARD/)
             Peptide
                                                               Protein
                                                                                                                                                                                                                                KRON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Compounds of the structure or formula 5-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH): L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-FP) (1-34); R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity,
                                                                                                                                                                                                                                                             increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutant parathyroid hormone (PTH) receptor designated rdeltaNt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant; parathyroid hormone; PTH; receptor; rdeltaNt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 21; I
Pred. No. 8.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 8.1 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
23..435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB07529 standard; Protein; 435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 YFLATNYYWILVEGLYLH 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand binding domain.
                                                                                                                                                                                                                                                                                                                                                                                               435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB07529;
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Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH[1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PFHFP which avoids the need for regular injections to treat osteoporosis.
                                                                                                                                                                                                                                                                                       New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTH; parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 21; Length 446;
Pred. No. 8.3e-10;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..23
/label= Signal_sequence
/note= "Human PTH-1 receptor residues 1-23"
24..32
                                                                                                                                                                                                 Jueppner H;
                                                                                                                                                                                               Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tethered PTH-1 receptor, Tether1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96986 standard; Protein; 448 AA.
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/label= PTH(1-9)
33..36
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.2
100.0%; Pr.
0;
                                                                                                                                                                                                                                                                                                                                                              Claim 22; Fig 7; 119pp; English.
                                                                                                                                                                                                 Kronenberg HM,
                                     99WO-US31108
                                                                      98US-0114577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3 Best Local Similarity 100. Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Homo sapiens.
                                                                                                        GARDELLA T J.
KRONENBERG H
                                                                                                                                                                                                                                   WPI; 2000-452384/39.
N-PSDB; AAA51732.
                                                                                                                                           (POTT/) POTTS J T. (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 AA;
                                                                                                                                                                                               Gardella TJ,
                                   30-DEC-1999;
                                                                    31-DEC-1998;
06-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                        (GARD/) (KRON/) H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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ID AAY9
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                                                                                                                                                                                                                                                                                                      New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTH; parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a mutant parathyroid hormone (PTH receptor, designated rdeltaNt. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists and antagonists of PTH receptor
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0
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/label= PTH-1_receptor_signal_sequence
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/label= PTH_residues_1-9
33..36
/label= linker
37..446
/label= PTH-1_receptor
/note= "residue 182 to end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preq. N. +ive 0; Mismatches
/note= "mature protein"
                                                                                                                                                                                                                  Potts JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96983 standard; Protein; 446 AA.
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                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 1; 81pp; English.
                                                                                                                                                                                                              Gardella TJ, Kronenberg HM,
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                                                                                                                                         98WO-US27862
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                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                              PTH receptor activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Rattus sp.
                                                                                                                                                                                                                                                WPI; 2000-465971/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 AA;
                                                                                                                                                                                                                                                                      N-PSDB; AAA58932
                                 WO200040698-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200039278-A2
                                                                                                        31-DEC-1998;
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                                                                    13-JUL-2000
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity
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Peptide
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18

õ g RESULT 1

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Gaps

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/label= Signal_sequence
/note= "Human PTH-1 receptor residues 1-23"
                                                                                                                                                                                                                                   (POTT/) POTTS J T. (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAA51737.
                                                                                                                  WO200039278-A2.
                                                                                                                                                                30-DEC-1999;
                                                                                                                                                                                     31-DEC-1998;
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                                                                                                                                         06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY99600;
                                                                                                                                                                                                            GARD/)
                          Peptide
                                                Peptide
                                                                      Protein
                                                                                                                                                                                                                        KRON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY99600
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                          Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the PTH-r receptor signal sequence; and R is (a portion of) PTH-receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis.
                                                                                                                                                                                                                                                         New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
37..448
/label= PTH-1_receptor
/note= "Human PTH-1 receptor residues 182-593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.3%; Score 18; DB 21; Length 448; 100.0%; Pred. No. 8.3e-10; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                 Potts JT, Jueppner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tethered PTH-1 receptor, Tether-R11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96988 standard; Protein; 450 AA.
                                                                                                                                                                                                                                                                                                      Example 4; Fig 17; 119pp; English
                                                                                                                                                                                                Sardella TJ, Kronenberg HM,
                                                                                                                 98US-0114577.
                                                                                           99WO-US31108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Homo sapiens.
                                                                                                                                         GARDELLA T J.
KRONENBERG H M.
                                                                                                                                                                                                                       WPI; 2000-452384/39.
                                                                                                                                                                          (JUEP/) JUEPPNER H.
                                                                                                                                        (GARD/) GARDELLA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 AA;
                                                                                                                                                                POTTS J T
                                                                                                                                                                                                                                  N-PSDB; AAA51735
                                             WO200039278-A2
                                                                                                                 31-DEC-1998;
                                                                    06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Peptide
  Protein
                                                                                                                                                   (KRON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
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Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R.l is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence; and R is (a portion of) PTH-1 receptor sequence; no mew compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetheri activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHRP which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound comprising an amino terminal signaling functional domain
linked to a carboxy-terminal binding portion of parathyroid hormone for
treating mammalian conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zebrafish; parathyroid hormone type-1 receptor; PTH1R; developmental disorder; physiological disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                           /note= "Human PTH-1 receptor residues 182-593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avoids the need for regular injections to treat osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 18; DB 21; Length 45
100.0%; Pred. No. 8.4e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potts JT, Jueppner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zebrafish parathyroid hormone type-1 receptor PTH1R.
                                                                          35.38
/label= Linker
39.450
/label= PTH-1_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY99600 standard; Protein; 536 AA.
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24..34
/label= PTH(1-11)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0114577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US31108
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARDELLA T J.
KRONENBERG H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-452384/39.
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This sequence is a parathyroid hormone receptor type 1 (PTHIR)
receptor protein of the invention. The invention also relates to a PTH3R
receptor protein. Antagonists of PTHIR or PTH3R can be used for the
treatment of diseases associated with an increase in PTHIR or PTH3R
activity, respectively. The peptides are used for diagnosis or prognosis
of diseases and disorders associated with PTH3R or PTHIR, such as cancer.
The polypeptides can be used as a molecular weight markers on sodium
dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
molecular sieve gel filtration columns. Antigenic epitope-bearing
on molecular sieve gel filtration columns. Antigenic epitope-bearing
peptides and polypeptides are useful to raise antibodies, including
monochonal antibodies, that bind specifically to a polypeptide. The
peptides are useful during diagnosis of diseases and disorders in
mammals involving PTHIR or PTH3R receptor expression or function.
Mutations that affect PTHIR or PTH3R sequence and/or expression levels
of PTH3R or PTH3R could be diagnostic for patients with disease or
                                                                                                Novel zebrafish parathyroid hormone/parathyroid hormone related peptide receptor 3 and isolated nucleic acid encoding zebrafish parathyroid hormone receptor 1 for treating disorders associated with receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders of a developmental, physiological or neurological nature. nucleic acid molecules are valuable for chromosome identification. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mapping of DNAs to chromosomes is an important first step in correlating those sequences with genes associated with disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat bone PTH/PTHrP receptor clone R15B prod.
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                                                                                                                                                                                                     Claim 17; Fig 2a; 111pp; English.
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100.0%; Prr
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92US-0864475.
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Rubin DA;
                                    WPI; 2000-412319/35.
N-PSDB; AAA30828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 AA;
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Jueppner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                function
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the parathyroid hormone type-1 receptor (PTHIR) from the zebrafish. Its coding seequence was obtained by sequencing a cDNA clone. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer; parathyroid hormone type 1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding parathyroid hormone receptors PTHIR and PTHIR, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 9.8e-10;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zebrafish PTH1R receptor protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Fig 2A; 111pp; English.
                                                                                                                                         99WO-US28207
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                    Jueppner H, Rubin DA;
                                                                                                                                                                                                                                                                                                                           WPI; 2000-412323/35.
N-PSDB; AAA49625.
                                                                                                                                                                                                                        JUEP/) JUEPPNER H.
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                                                                                                                                                                                                                                              (RUBI/) RUBIN D A.
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                   Brachydanio rerio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification.
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                                                         WO200032775-A1
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                                                                                                                                       30-NOV-1999;
                                                                                                                                                                               30-NOV-1998;
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                                                                                                08-JUN-2000
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Gaps
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3.3%; Score 18; DB 21; Length 536; 100.0%; Pred. No. 9.8e-10; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parathyroid hormone; related protein; calcium; antagonist; antibodies; hypercalcaemia.
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AAY90230

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05-APR-1991;
                                                                                                                                                                                      06-APR-1992;
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                                                                                                                         US5494806-A.
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                                                                                                                                              27-FEB-1996
                                                                                                                                                                                                                                                                                                                              cancer etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW73316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
             Region
                               Region
                                                    Region
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AAW73316
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                                                                                    The rat bone parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP) receptor protein sequence was deduced from close RISB obtd. by screening a rat osteosarcome (ROS) cell cDNA library to isolate those expressing functionally intact PTH/PTHFP receptor proteins, performed according to Gearing et al., (EMBO J. 8: 3676, 1989), by identifying colonies capable of binding a suitable readio. Labelled ligand. The protein may be used in a therapeutic compsn. to inhibit activation of PTH or PTHFP and thus reduce the level of calcium in the blood. Cpds. capable of competing with PTH or PTHFP for binding can be identified using the protein and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment. Classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in See also AAR27704-16.
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                                                                                                                                                                                                                                                                                                                   Gaps
                             New DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer.
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                                                                                                                                                                                                                                                                                           3.3%; Score 18; DB 13; Length 591; 100.0%; Pred. No. 1.1e-09; ive 0; Mismatches 0; Indels
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/label= Extracellular_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193..211
/label= Transmembrane_region
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'label= Intracellular_region
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365..383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            AAR92277 standard; Protein; 591 AA.
                                                                     Claim 20; Fig 3; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat bone PTH/PTHrP receptor.
                                                                                                                                                                                                                                                                                                                                     245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                              290 yflatnyywilveglylh 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212..221
/label= In
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/label- T1
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/label= Ex
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/label- Ti
                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .364
                                                   and treatment of tumours
WPI; 1992-366271/44.
N-PSDB; AAQ29606.
                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                             591 AA;
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                                                                                                                                                                                                                                                                                           Query Match
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Region
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding vertebrate parathyroid hormone receptor - useful for diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
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'label= Transmembrane_region
                                                     Intracellular_region
                                                                                                                /label= Transmembrane_region
                                                                                                                                        429..444
/label Intracellular_region
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/label= Intracellular_region
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Schipani E, Segre GV;
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91US-0681702.
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Matches 18; Conservative
                             384..408
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This sequence represents the human parathyroid hormone (PTH) receptor which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or
                                                                                                                                                                                                                        A human parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) receptor (AAR92278) is encoded by CDNA clone HK-1 (AAT15948) isolated from a human kidney cDNA library. The receptor induces an increase in intracellular cAMP and intracellular free calcium when challenged by PTH or PTHrP. Recombinant receptor can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host cells PTH serum levels.
                                                                          DNA encoding vertebrate parathyroid hormone receptor - useful for diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
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Pred. No. 1.1e-09;
0; Mismatches 0;
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100.0%; Prr
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95US-0471494.
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  WPI; 1996-139028/14.
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N-PSDB; AAV08391.
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Best Local Similarity
Matches 18; Conserv
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Schipani E, Segre
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                        N-PSDB; AAT15948
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06-JUN-1995;
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therapeutic
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Schipani E, Segre GV;
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91US-0681702.
95US-0471494.
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05-APR-1991;
06-JUN-1995;
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opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies and GPCR antagonists may also be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR polypeptides in samples.
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTRR; hi5571; immunomodulatory; vascular; hepatic; antiasthma; antimicrobial; antiinflammatory; immunosuppressive; gene therapy; vascine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoImmunity; graft rejection; cystic fibrosis.
                                                                                                                                                                       ;
                                                                                                                                 Length 593;
                                                                                                                                                                    Indels
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                                                                                                                                 Score 18; DB 20; I
Pred. No. 1.1e-09;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PTRR seven transmembrane domain.
                                                                                                                                                                                                                                                                                                                                      AAB71876 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 145pp; English.
                                                                                                                                     100.08; Pic
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                                                                                                                                 3.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1999; 99US-0146916.
29-FEB-2000; 2000US-0515781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000; 2000WO-US21278.
                                                                                                                                                                                                        245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                Best Local Similarity 100.
Matches 18; Conservative
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                                                                           593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200109328-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                          AAB71876;
                                                                             Sequence
                                                                                                                                   Query Match
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein sequence was deduced from the cDNA sequence obtd by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schipani
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         Length 593;
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                                                                                                                                                                                                                                                                                          Parathyroid hormone; related protein; calcium; antagonist;
         Score 18; DB 22; Length 59
Pred. No. 1.1e-09;
); Mismatches 0; Indels
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Pred. No. 1.1e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Juppner H, Kronenberg HM,
                                                                                                                                                                        AAR27707 standard; Protein; 614 AA.
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100.0%; Pre
0;
3.3%; Scc...
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligand such as in hypercalcaemia.
                                                                                                                                                                                                                                                               Human kidney PTH/PTHrP receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Fig 6; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0681702.
92US-0864475.
                                                                  245 YFLATNYYWILVEGLYLH 262
                                                                                   245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                           antibodies; hypercalcaemia.
                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-366271/44.
N-PSDB; AAQ29607.
          Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 AA;
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                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                   W09217602-A.
                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1992.
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WPI; 1996-139028/14.
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                 05-APR-1991;
                                                                                                                                                     06-APR-1992;
05-APR-1991;
                                                                                          US5494806-A.
                                                                                                              27-FEB-1996.
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PTH-related
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                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                             parathyroid hormone/parathyroid hormone related protein tragment of parathyroid hormone related protein.

(PTH/PTHFP) receptor protein. The peptide is capable of binding PTH or PTHFP and acting as an antagonist of these cpds. The peptide may be used to inhibit activation of PTH or PTHFP and thus reduce the level of calcium in the blood. Cpds. capable of competing with PTH or PTHFP for binding can be identified using the protein prod. and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also AAR27704-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      peptide sequence shown represents an extracellular fragment of
                                                                                                                                                                                                                                                                                                                                                           New DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis
                                                                                                                                                                                                                                                                                                          Schipani E;
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0
                                                                                                                                           Parathyroid hormone; related protein; calcium; antagonist; antibodies; hypercalcaemia; extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
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6.1e-07;
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                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
                                                                                                                                                                                                                                                                                                          Kronenberg HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92281 standard; Peptide; 19 AA.
                                                          AAR27710 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6%; Scur
100.0%; Pre
0; }
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                                                                                                                                                                                                                                    92WO-US02821
PTH/PTHrP receptor fragment
                                                                                                                                                                                                                                                      91US-0681702
92US-0864475
                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                         Juppner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.6
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 YFLATNYYWILVEG 258
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                                                                                                  16-MAR-1993
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06-APR-1992;
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                                                                                                                                                                                           W09217602-A
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                                                                                                                                                                         Synthetic.
                                                                               AAR27710;
                                                                                                                                                                                                                                                                                                                  Segre GV;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding vertebrate parathyroid hormone receptor - useful for diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
                                                        Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%; Score 14; DB 17; 1
100.0%; Pred. No. 6.1e-07;
tive 0; Mismatches 0;
PTH/PTHrP extracellular region fragment RP-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kronenberg HM,
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Schipani E, Segre GV;
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Disclosure; Fig 2; 145pp; English.
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N-PSDB; AAQ89546.
                                                                                                                                                                                                                                           Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                     457 AA;
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                                                                                                                                                                                                                                                                                                                                                                 AAR72506;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                    This sequence is a fragment of a opossum parathyroid hormone (PTH) receptor which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; h15571; immunomodulatory; vascular; hepatic; antiasthma; VIPR; pitultary adenylate cyclase activating polypeptide type II receptor; antimicrobala; antiinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease, organ-specific autoimmunity; graft rejection; cystic fibrosis.
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                           Antibody to parathyroid hormone receptor - for diagnostic or
therapeutic use
                                                                                                                                                                                                                                                                        Score 14; DB 20; Length 19;
Pred. No. 6.1e-07;
); Mismatches 0; Indels
                                                                    Potts JT;
                                                                  Juppner H, Kronenberg HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human VIPR seven transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                   AAB71878 standard; Protein; 457 AA.
                                                                                                                                                 Claim 8; Column 19; 63pp; English.
                                                                                                                                                                                                                                                               2.6%; Scur-
100.0%; Prev
0; }
        92US-0864475.
91US-0681702.
95US-0471494.
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                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-2001 (first entry)
                                                (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                              245 YFLATNYYWILVEG 258
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                                                                             Segre GV;
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                                                                                               WPI; 1999-034124/03
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                                                                                                                                                                                                                                          19 AA;
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                                                                   Abou-Samra A,
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        06-APR-1992;
05-APR-1991;
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                           06-JUN-1995;
                                                                             Schipani E,
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                                                                                                                                                                                                                                                                                                                                                                                                        AAB71878;
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                        Query Match
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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h15571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, hemantological, fibroic, hepatic and respiratory discorders including asthma, allergies (e.g. allergic and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies and GPCR antagonists may also be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR.
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[00.0%; Pred. No. 0.00011;
[ve 0; Mismatches 0; Indels
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            NAME OF THE PROOF 
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sequencing. Thereafter the gene was inserted into the plasmid pRC/CMV for transfection of 293 cells and production of the recombinant protein. The activity of pVIP is linked to vasodilation in the lungs and gastrointestinal tract. The receptor is useful in a bioactivity assay for quantifying the level of stimulation and repression of pVIP enzymatic activity in response to test compounds. The receptor is also useful in screening for pVIP receptor inhibitory or stimulatory agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasoactive intestinal polypeptide receptor; VIP; rat; binding; adenylate cyclase activity; stimulus.
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                                                                                                                                                                                                                                                                                                                                      Length 458;
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                                                           Human glucose-dependent insulinotropic peptide receptor protein sequence.
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                                                                                                                   Human; glucose-dependent insulinotropic peptide receptor; GIPR;
GIP receptor; osteotropic hormone; bone; osteoblast; osteoporosis;
bone density; bone formation.
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98DE-1036382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel recombinant GIP (Glucose-dependent insulinotropic/insulin releasing polypeptide) receptor protein (I) or an active fragment of (I), which binds to the GIP peptide hormone without initiating a signal transduction cascade. The invention also describes a (1) a recombinant DNA molecule (II), encoding (I) or its active fragment, comprising: (a) a promoter that is in the beta cells of the pancreas; (b) a sequence that is capable of binding to the GIP peptide hormone without initiating a signal transduction cascade; (c) a termination sequence; and (d) a polyadenylated tail sequence, where the expression of (II) in a sultable host causes a diabetes type phenotype. (2) a vector (II), comprising (II); (3) a eukaryotic or prokaryotic cell line (IV), containing (II); and (5) preparing (V). (V) is used as a model system for the investigation of the development, treatment and consequences of the investigation of the development, treatment and consequences have been developed, but the use of (I) in a transgenic animal demonstrates of the role of a defective GIP receptor in the development of diabetes, which has not been shown before. This sequence represents the human GIP receptor protein varaint which has a deleted intracellular loop
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                                                                                                                                                                                                                                                                                           Recombinant GIP (Glucose dependent insulinotropic polypeptide) receptor protein used as a model for investigation of development and treatment of diabetes mellitus.
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                                                                                                                                                                                                                   Wolf E;
                                                                                                                                                 (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI
                                                                                                                                                                                                                 Goeke B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY51526 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 11-12; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Procest Processing Proce
                                                                                                                                                                                                                 Volz A,
                                                                                                      98DE-1036382.
                                                             99EP-0115140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-0115140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2000 (first entry)
                                                                                                                                                                                                                 Peters H, Balling R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 FRRLHCTRNYIH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-162923/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 458 AA;
                                                                                                                                                                        (WOLF/) WOLF E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIP receptor;
                                                             11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-1999;
                                                                                                      11-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                  16-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP979872-A1
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This invention describes a novel recombinant GIP (Glucose-dependent insulinotropic/insulin releasing polypeptide) receptor protein (I) or an active fragment of (I), which binds to the GIP peptide hormone without initiating a signal transduction cascade. The invention also describes a (I) a recombinant DNA molecule (II), encoding (I) or its active fragment, comprising: (a) a promoter that is in the beta cells of the pancreas; (b) a sequence that is capable of binding to the GIP peptide hormone without initiating a signal transduction cascade; (c) a termination equence; and (d) a polyadenylated tail sequence, where the expression of (III), comprising (II); (3) a eukaryotic or prokaryotic cell line (IV), containing (II); (4) a transgenic, non human animal (V), containing (II); (d) a eukaryotic or prokaryotic cell line (IV), containing (II) or (III); (4) a transgenic, non human animal (V), containing (II) and (5) preparing (V); (V) is used as a model system for the investigation of the development, treatment and consequences of diabetes mellitus. Several animal models for the study of diabetes have the role of a defective GIP receptor in the development of diabetes, which has not been shown before. This sequence represents the human GIP (V), receptor protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                Recombinant GIP (Glucose dependent insulinotropic polypeptide) recepton protein used as a model for investigation of development and treatment
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(GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
                                                                                                                                Volz A, Goeke B, Wolf E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human GIPR seven transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 9-10; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB71870 standard; Protein; 466 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luv...
..... 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         of diabetes mellitus -
                                                                                                                       Peters H, Balling R,
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                                                                                                                                                                                                                WPI; 2000-162923/15.
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New nucleic acid encoding vasoactive intestinal peptide receptor
             and related polypeptides, vectors, transformed cells, probes and antibodies, useful for diagnosis and for screening potential
                                                           Disclosure; Figure 3; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY90231 standard; Protein; 523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 38; Fig 2b; 111pp; English.
                                                                                                                                                                                                                                                                                    99WO-US11883
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                                   agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jueppner H, Rubin DA;
                                                                                                                                                                                                                                                                                                                                     250 NYYWILVEGLY 260
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                                                                                                                                                                                                                                                                                                                                                   1 nyywilvegly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RUBI/) RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio.
                                                                                                                                                                                                                                                      11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90231;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function
                                                                                                                                                                                                                                 claimed
                                                                                                                                                                                                                                                                                                                                                                                                 41
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ID AAY9
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                                                                                                                                                                           The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h15571. h15571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory diseases including asthma, allergies fraintis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies may be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR.
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                                                                                                        Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretin family; G-protein linked receptor; transmembrane domain.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Opossum parathyroid hormone transmembrane domain.
                                                                                                                                                       Disclosure; Fig 2; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR70138 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     West KM;
                                   (MILL-) MILLENNIUM PHARM INC.
03-AUG-1999; 99US-0146916.
29-FEB-2000; 2000US-0515781.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                              polypeptides in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 FRRLHCTRNYIH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harmar AJ, Lutz EM,
                                                          Hodge MR, Lloyd C,
                                                                                WPI; 2001-138653/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-115440/15
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                                                                                                                                                                                                                                                                                                                                                                                     466
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
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Matches
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Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer; parathyroid hormone type 1 receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel zebrafish parathyroid hormone/parathyroid hormone related peptide receptor 3 and isolated nucleic acid encoding zebrafish parathyroid hormone receptor 1 for treating disorders associated with receptor
                              VIP2 receptor was identified by PCR of rat pituitary cDNA using degenerate oligo primers corresp. to the third and seventh transmembrane domains of the secretin family of G-protein linked receptors (Q83212 and Q83213 respectively). The primers were based on the third and seventh transmembrane domains of the rat secretin, pig calcitonin and opossum parathyroid hormone (PTH) receptors (see R70137-R701410. Full length cDNAs were isolated from an olfactory bulb cDNA library. The sequence has been submitted to the EMBL/GenBank database under accession No. 225885 (see Q83211/R70136). A polynucleotide probe comprising a labelled DNA or RNA sequence capable of specifically binding to a gene for VIP2 receptor is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
VIP2 is an adenylate cyclase-linked VIP receptor from rat brain. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 11;
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treceptor protein. Antagonists of PTHIR or PTHIR can be used for the treatment of diseases associated with an increase in PTHIR or PTHIR or activity, respectively. The peptides are used for diagnosis or prognosis of diseases and disorders associated with PTHIR or PTHIR, such as cancer. The polypeptides can be used as amolecular weight markers on sodium docerns in the polypeptides are useful columns. Antigenic epitope-bearing peptides and polypeptides are useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide. The peptides are useful during diagnosis of diseases and disorders in mammals involving PTHIR or PTHIR receptor expression or function. Mutations that affect PTHIR or PTHIR sequence and/or expression levels of prints or PTHIR could be diagnostic for patients with disease or disorders of a developmental, physiological or neurological nature. The mapping of DNAs to chromosome for chromosome identification. The mapping of DNAs to chromosomes as an important first step in correlating those sequences with genes associated with disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zebrafish; parathyroid hormone type-3 receptor; PTH3R;
developmental disorder; physiological disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding parathyroid hormone receptors PTHIR and PTHIR, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 11; DB 21; Length 523;
100.0%; Pred. No. 0.014;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zebrafish parathyroid hormone type-3 receptor PTH3R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 ywilveglylh 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 YWILVEGLYLH 262
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RUBI/) RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                            523 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid hormone (PTH) receptor fragments, including those (AAR92229-84) based on the PTH extracellular region and those (AAR92286-87) based on the intracellular domain, are produced by incorporating encoding DNA sequences into a vector, and culturing cells transformed by the vector. The peptides can be used to raise antibodies. The peptides and antibodies are useful in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, and can also be used to screen for (ant)agonists of therapeutic appln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding vertebrate parathyroid hormone receptor - useful for diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
be used to identify agonists and antagonists which can be used in similar manner. In addition, the gene can be used for chromosome
                                                                                                                                                                                                                                                                                                                                                                                      parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer.
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                                                                                             2.0%; Score 11; DB 21; Length 542;
100.0%; Pred. No. 0.015;
                                                                                                                              Indels
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0
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100.0%; Pred. No. 0.0043;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          Parathyroid hormone; receptor; parathormone; PTH;
                                                                                                                                                                                                                                                                                                                                             PTH/PTHrP intracellular region fragment RPi-7.
                                                                                                               100.0%; Pred. No. 0.0
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juppner H, Kronenberg HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 3; 64pp; English.
                                                                                                                                                                                                                                                         AAR92285 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0681702.
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91US-0681702
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP.
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                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abou-Samra A, Juppue.
                                                                                                                                                                         1111111111
236 ywilveglylh 246
                                                                                                                                                          252 YWILVEGLYLH 262
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 FRRLHCTRNY 178
                                                                                                               Best_Local Similarity
Matches 11; Conserv
                                                        542 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
                            identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1991;
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                                                                                                                                                                                                                                                                                                                18-MAY-1996
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                                                        Sequence
                                                                                                                                                                                                                                                                                      AAR92285;
                                                                                                  Query Match
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This is a human glucagon-like peptide-2 (GLP-2) receptor fragment. The specification provides the sequences of human and rat GLP-2 receptors. Genetically engineered host cells containing the GLP-2 receptor encoding nucleic acid sequences operably linked to expression elements can be used to produce the recombinant proteins. These cells can be used in a method for identifying GLP-2 receptor ligands which comparises incubating a candidate ligand with the cell, and determining whether binding has occurred between the GLP-2 receptor and the candidate ligand. The GLP-2 receptor and the candidate ligand. The GLP-2 receptor solvents of the GLP-2 receptor and second the candidate ligand as the GLP-2 receptor and second of solutions. They can also be used for constructing cell lines for GLP-2 receptor ligand screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; human; glucagon receptor; transgenic animal; metabolism; model; signal sequence; transmembrane domain; glycosylation site.
                                                                                                                                                                                                                                                                                                                                                                              New, e.g. rat glucagon-like peptide-2 receptor - useful for, isolating homologues and GLP-2 receptor ligand screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19; Length 222;
. 0.07;
ches 0; Indels
                                                                                                                                                                                                                                                                                         Vyas TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 10; DB
100.0%; Pred. No. 0.0
iive 0; Mismatches
                                                                                                                                                                                                                                                                                       Fan E, Gupta AK, McCallum K, Munroe DG,
                                                                                                                                                                                                                                                   (ALLX ) ALLELIX BIOPHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR50047 standard; Protein; 477 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                             97US-0845546.
96US-0767224.
97US-0787721.
                                                                                                                                             97WO-CA00969
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 receptor ligand screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human glucagon receptor.
                                                                                                                                                                                                                                                                                                                        WPI; 1998-34849/30.
N-PSDB; AAV39157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 LHCTRNYIHM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 AA;
                                       Homo sapiens
                                                                      WO9825955-A2
                                                                                                                                             15-DEC-1997;
                                                                                                                                                                                                 13-DEC-1996;
24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-1992;
01-JUL-1993;
                                                                                                                                                                                24-APR-1997;
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                                                                                                          18-JUN-1998
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                                                                                                                                                                                                                               Rat; human; glucagon receptor; transgenic animal; metabolism; model; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant glucagon receptors and antibodies - useful to produce model transgenic animals for study and with therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5 describes the isolation of human GR.
The GR coding sequence was constructed from partial clone
p9A11 (5' end) and clone 40.2-2 (3' end).
Host cells conty GR DNA may be used for the prodn. of
recombinant GR. GR DNA may also be expressed in non-human
transgenic animals, pref. mice.
Such animals may be readily
used as models to study the role of the glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 10; DB 15; Length 162;
100.0%; Pred. No. 0.053;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human glucagon-like peptide-2 (GLP-2) receptor fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jelinek LJ, Kindsvogle WR;
'Hara PJ, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 86-87; 112pp; English.
                                                                                                                                                                                             Human GR C-terminal (clone 40-2-2).
                                                                                     AAR57829 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW68067 standard; Protein; 222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Hara PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0938331.
93US-0086631.
                                                                                                                                                                                                                                                                                                                                                                                               93WO-US08174.
                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grant FJ,
Lok S, O'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-101194/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ67247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In metabolism.
                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993;
                                                                                                                                                                                                                                                                                                                      WO9405789-A
                                                                                                                                                              03-OCT-1994
                                                                                                                                                                                                                                                                                                                                                            17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuijper JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foster DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                        AAR57829;
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AAW68067 RESULT

XX BX BX BX XX

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Gaps

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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR cost designated h15571. h1571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, hemmatological, fibrotic, hepatic and respiratory discorders including asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, or graft rejection, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies and ablants GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies and GPCR antagonists may be used as diagnostic agents for detecting the presence of GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This represents a rat glucagon-like peptide-2 (GLP-2) receptor. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat; receptor ligand screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat glucagon-like peptide-2 receptor - useful for, homologues and GLP-2 receptor ligand screening
                                                                                                                                                                                                                                                                                                                                                                                   Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vyas TB;
                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 10; DB 22;
100.0%; Pred. No. 0.14;
iive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat glucagon-like peptide-2 (GLP-2) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Munroe DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW68066 standard; Protein; 550 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gupta AK, McCallum K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Fig 2; 54pp; English
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97US-0787721
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                          polypeptides in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67..550
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N-PSDB; AAV39156.
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243 lveglylhnl 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 LVEGLYLHNL 264
                                                                                                                                                                                                                                                                                                                             477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09825955-A2
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24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW68066;
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fan E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW68066
       QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; GLR: glucagon receptor; h15571; immunomodulatory; vascular; hepatic; antiasthma; anitmicrobial; antinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoimmunity; graft rejection; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                           New recombinant glucagon receptors and antibodies - useful to produce model transgenic animals for study and with therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                      Rat and human glucagon receptor (GR) DNA was isolated.
Host cells contg. GR DNA may be used for the prodn. of
recombinant GR. GR DNA may also be expressed in non-human
transgenic animals, pref. mice. Such animals may be readily
used as models to study the role of the glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                           , Jelinek LJ, Kindsvogle WR;
O'Hara PJ, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.14;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 10; DB
100.0%; Pred. No. 0.1
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human GLR seven transmembrane domain.
                                                                                                                                                                                                                                                    Claim 4; Page 91-95; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB71872 standard; Protein; 477 AA.
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29-FEB-2000; 2000US-0515781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                       (ZYMO ) ZYMOGENETICS INC.
                                                             Grant FJ,
                                                                                Lok S,
                                                                                                                  WPI; 1994-101194/12.
N-PSDB; AAQ58776.
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                                                                                                                                                                                                                   applications
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                                                                                Kuijper JL,
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                                                             Foster DC,
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AAB71872 RESULT

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specification provides the sequences of human and rat GLP-2 receptors. Genetically engineered host cells containing the GLP-2 receptor encoding nucleic acid sequences operably linked to expression elements can be used to produce the recombinant proteins. These cells can be used in a method for identifying GLP-2 receptor ligands which comprises incubating a candidate ligand with the cell, and determining whether binding has occurred between the GLP-2 receptor and the candidate ligand. The GLP-2 receptor polynucleotides can be used to isolate GLP-2 receptor-encoding homologues. They can also be used for constructing cell lines for GLP-2
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                                                                                                                                                                                                                            1.8%; Score 10; DB 19; Length 550;
100.0%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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96US-0767224.
97US-0787721.
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                                                                                                                                                receptor ligand screening.
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Les 10; Conservative
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N-PSDB; AAV39155.
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206 lhctrnyihm 215
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13-DEC-1996;
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occurred between the GLP-2 receptor and the candidate ligand. The GLP-2 receptor polynucleotides can be used to isolate GLP-2 receptor-encoding homologues. They can also be used for constructing cell lines for GLP-2 receptor ligand screening.
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                                                                                                                   DB 19; Length 553;
0.16;
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Compugen Ltd.
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protein search, using sw model OM protein

; Search September 21, 2001, 17:08:32 Run on:

alignments) Million cell updates/sec (without a 2102.573 P

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US-09-236-468A-2 541 1 MAWLGASLHVWGWLMLGSCL......DDILMEKPSRPMESNPDTEG Title: Perfect score: Sequence:

541

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

17

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	parathyroid hormon	parathyroid hormon	secretin receptor	secretin receptor	parathyroid hormon	parathyroid hormon	parathyroid hormon	parathyroid hormon	qastric inhibitory	vasoactive intesti	vasoactive intesti	qastric inhibitory	vasoactive intesti	qastric inhibitory	qlucose-dependent	glucose-dependent	glucagon receptor
QI	A57519	A39286	JC2532	S16319	159297	S44203	I54195	A49191	153273	JH0594	JC2194	JC2462	JC2195	G02234	S66676	137411	JC2041
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Query Match Length DB	550	585	440	449	589	591	591	593	455	459	460	462	495	466	466	491	477
Query	67.1	4.6	3.5	3.5	3.3	3.3	3.3	3.3	2.4	2.4	2.4	2.4	2.4	2.2	2.2	2.2	1.8
Score	363	25	19	19	18	18	18	18	13	13	13	13	13	12	12	12	10
Result No.	н	7	Э	4	5	9	7	80	σ	10	11	12	13	14	15	16	17

ALIGNMENTS

parathyroid hormone receptor 2 precursor - human N;Alternate names: PTH2 receptor C;Species: Homo sapiens (man) C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999 C;Accession: A57519

ATHILE: Identification and functional expression of a receptor selectively recognizing the ference number: A57519; MUID:95318121
A; Reference number: A57519; MUID:95318121
A; Actatus: preliminary; nucleic acid sequence not shown a; Molecule type: mRNA
A; Residues: 1-550 < USD>
A; Charles: preliminary; nucleic acid sequence not shown a; Molecule type: mRNA
A; Residues: 1-550 < USD>
A; Cenetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Genetics: C; Genetics: C; Cyperion: 2433-2433
A; Csuperfamily; glucagon receptor C; Keywords: hormone receptor ö FVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMF 243 423 64 FPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYS 123 DCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIHMHL 183 244 IYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLAD 303 Gaps 4 LGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNC 63 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAE ö 1; Indels Length VKKMWSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAA 467 5 Score 363; DB Pred. No. 0; 0; Mismatches DB 67.1%; 99.8%; Query Match 67.1 Best Local Similarity 99.8 Matches 463; Conservative 184 9 124 124 184 364 364 424 424 g ð ò q ò qq ò Op ò g ð g δ pp ŏ qq

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parathyroid hormone and parathyroid hormone-

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RESULT 6
544203
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Dete: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C;Accession: 544203
R;Karperien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boon submitted to the EMBL Data Library, April 1994
A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related
A;Reference number: 544203
A;Accession: 544203
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Nug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C;Accession: I54195; A42698
R;Pausova, Z; Bourdon, J; Clayton, D; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Riv
Genomics 20, 20-26, 1994
A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide recepto
and rat genomes.
A;Reference number: I54195; MUID:94292182
                                                        Rinccuig, K.A.; Clarke, J.C.; White, J.H.

Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994

A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathy A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathy A:Title: Molecular i19297; MUID:94255468

A:Steference number: 159297

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Residues: 1-589 <RES>

A:Cross-references: GB:L34611; NID:9530149; PIDN:AAA40011.1; PID:9530151
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R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.;
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyr of both cAMP and inositol trisphosphates and increases intracellular free calcium.
                                                                                                                                                                                                                                                                                                                                                    A;Gene: PTHR
A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C;Superfamily: glucagon receptor
        C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
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A; Residues: 1-591 <KAR>
A; Cross-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
C; Superfamily: glucagon receptor
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Pred. No. 7.3e
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C.Accession: S16319
R.Ishihara, T.: Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A.Title: Molecular cloning and expression of a cDNA encoding the secretin receptor. A; Reference number: S16319; MUID:91266890
A.Reference. S16319
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                            C, Jano, S. 13-railist Fsequence_revision 11-Apr-1997 #text_change 05-Nov-1999 C, Accession: 022532
R: Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A; Ittle: Molecular cloning and functional expression of a human pancreatic secr. A; Reference number: JC2532; MUD:95169147
A; Accession: JC2532
A; Status: nucled.c acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-440 <JIA>
A; Cross-references: EMBL:U20178; NID:9662795; PIDN:AAC50106.1; PID:9662796
A; Experimental source: pancreas
C; Genetics:
A; Genetics:
A; Genetics: A; A; Cross-references: GDB:270546; OMIM:182098
A; Map position: 2q14.1-2q14.1
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C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
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C;Species: Mus musculus (house mouse)
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100.0%; Pred. No. 5.5e-11;
ive 0; Mismatches 0; Indele
4.6%; Score 25; DB 2; Length 585;
Llarity 100.0%; Pred. No. 5e-17;
Conservative 0; Mismatches 0; Indels
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Pred. No. 5.4e-11;
0; Mismatches 0;
                                                                                                                    167 GYFRRLHCTRNYIHMHLFVSFMLRA 191
                                                                                                                                                  207 GYFREHCTRNYIHMHLFVSFMLRA 231
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Best Local Similarity 100.0%; P.
Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 FRRLHCTRNYIHMHLFVSF 185
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:Superfamily: glucagon receptor
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Best Local Similarity 100.0
Matches 19; Conservative
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  Query Match
Best Local Similarity
Matches 25; Conserv
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Gistric inhibitory polypeptide receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
C;Accession: 153273
R;Usdin, T.B.; Mazey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.
Endocrinology 133, 2861-2870, 1993
A;Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive A;Reference number: 153273; MUID:94062667
A;Steference number: 153273
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasoactive intestinal peptide receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: JH0594; S56014
R;Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A;Title: Functional expression and tissue distribution of a novel receptor for vasoac A;Reference number: JH0594; MUID:92232309
A;Accession: JH0594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Across-references: EMBL:U10635; NID:9505752; PIDN:AAB48185.1; PID:9514311
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein; p.130/Domain: signal sequence #status predicted <SIG>F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <TMI>F;146-168/Domain: transmembrane #status predicted <TMI>F;176-195/Domain: transmembrane #status predicted <TMI>F;218-241/Domain: transmembrane #status predicted <TMI>F;256-277/Domain: transmembrane #status predicted <TMI
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Biochem. J. 308, 719-723, 1995
Aritle: Characterization of the rat vasoactive intestinal polypeptide receptor gene
A;Reference number: S56014; MUID:97104266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;376-395/Domain: transmembrane #status predicted <TM7>
F;58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-459 <ISH>
A; Cross-references: GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
A; Experimental source: lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:L19660; NID:g431448; PIDN:AAC37637.1; PID:g431449
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F;344-363/Domain: transmembrane #status predicted <TM6>
F;376-395/Domain: transmembrane #status predicted <TM7>
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100.0%; Pred. No. 7.6e-05;
ive 0; Mismatches 0;
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                                                  290 YFLATNYYWILVEGLYLH 307
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Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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A; Residues: 1-455 <RES>
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A; Residues: 1-26 <PEI>
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A; Residues: 1-539 < RES.
A; Residues: 1-539 < RES.
A; Cross-references: EMBL:U22409; NID:g897594; PIDN:AAB60657.1; PID:g897596
B; Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V
B; Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V
B; Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V
A; Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
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C; Superfamily: glucagon receptor
C; Keywords: G protein-commission controls:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C; Accession: 138139; A49191: 138113; G01562; S29610
R; Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhrmann, M. Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
X-Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A; Title: Pseudohypoparathyroidism type Ib is not caused by mutations in the coding exons A; Reference number: 138139; MUID:95263723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parathyroid hormone/PTH-related peptide receptor - human
N.Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
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A; Residues: 1-593 <RE2>
A; Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
R; Levine, M
S; Levine, M
S; Levine, M
A; Reference number: G07787
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0
                                                                              A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-585, 'G', 587-591 <ABO>
A;Experimental source: ROS 17/2.8 osteosarcoma cells A;Note: sequence extracted from NCBI backbone (NCBIP:92187) C;Superfamily: glucagon receptor
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0. 7.3e-10; O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 591;
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100.0%; Pred. No. 7.3e-10;
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A; Reference number: A42698; MUID:92212903
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A;Molecule type: mRNA
A;Residues: 1-593 <LEV>
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A;Molecule type: mRNA
A;Residues: 1-593 <SCH>
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                                             A; Accession: A42698
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                             R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic isle
A;Reference number: JC2462; MUID:95110292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide receptor-related protein #status pred
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C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; stagedence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; stagedence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; stagedence_revision 07-Oct-1994
A;Reference number: JC2194; MUID:94235025
A;Accession: JC2195
                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-462 < YAS>
A; Cross-references: DBJ:D38103; NID:g644880; PIDN:BAA07284.1; PID:g765087
C; Superfamily: glucagon receptor
C; Superfamily: glucagon receptor
C; Keywords: receptor; transmembrane protein
F; 136-157/Domain: transmembrane #status predicted < YML>
F; 136-138/Domain: transmembrane #status predicted < YMZ>
F; 252-274/Domain: transmembrane #status predicted < YMA>
F; 272-274/Domain: transmembrane YMA>
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A;Experimental source: jejunal epithelial cell
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A:Map position: 3922-392
C.Superfamily: glucagon receptor
C:Superfamily: glucagon receptor
C:Superfamily: glucagon receptor
C:Superfamily: glucagon receptor
C:Reywords: glycoprotein: intestine; phosphoprotein; recept
F:1-31/Domain: signal sequence #status predicted <SIG>F:180-203/Domain: transmembrane #status predicted <TM1>F:211-229/Domain: transmembrane #status predicted <TM2>F:251-269/Domain: transmembrane #status predicted <TM3>F:251-269/Domain: transmembrane #status predicted <TM3>F:381-398/Domain: transmembrane #status predicted <TM6>F:381-398/Domain: transmembrane #status predicted <TM6>F:314-398/Domain: transmembrane #status predicted <TM6>F:314-398/Domain: transmembrane #status predicted <TM6>F:412-431/Domain: transmembrane #status predicted <TM7>F:412-431/Domain: transmem
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100.0%; Pred. No. 7.7e-05;
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N;Alternate names: GIP receptor
C;Species: Cricetinae gen. sp. (hamster)
C;Species: Ts-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
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Best Local Similarity
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preliminary; translated from GB/EMBL/DDBJ
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                          A; Molecule type: mRNA
A; Residues: 1-491 < RES.
A; Cross-references: EMBL: X81832;
C; Superfamily: glucagon receptor
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Best Local Similarity 100.
Matches 10; Conservative
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243 LVEGLYLHNL 252
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 LVEGLYLHNL 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C; Accession S66676
R; Volz. A.; Gocke, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Gocke, B.
FEBS Lett. 373, 23-29, 1995
A; Title: Molecular cloning, functional expression, and signal transduction of the GIP-re
A; Reference number: S66676; MUID:96013879
A; Accession: S66676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: glucagon receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-466/Product: glucose-dependent insulinotropic protein receptor #status predicted <M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rigremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens, E Diabetes 44, 1202-1208, 1995
A;Title: Cloning, functional expression, and chromosomal localization of the human pancr A;Reference number: 137411; MUID:96007224
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A;Molcoule type: manA
A;Residues: 1.466 <BON>
A;Residues: Leferences: EMBL:U39231; NID:91066050; PIDN:AAA84418.1; PID:91066051
                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C;Accession: G02234
R;Bonner, T.I.; Usdin, T.B.
R;Bonner, T.I.; October 1995
A;Reference number: G09336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose-dependent insulinotropic polypeptide receptor - human
C.Species: Homo sapiens (man)
C.Date: 12-Aug_1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.2%; Score 12; DB 2; Length 466; Best Local Similarity 100.0%; Pred. No. 0.00082; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB 2; Ler
Pred. No. 0.00082;
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                                                                             gastric inhibitory polypeptide receptor - human
N;Alternate names: GIP receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross references: GDB:335023
A)Map position: 19q13.3-19q13.3
C,Superfamily: glucagon receptor
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A; Residues: 1-466 <VOL>
A; Cross-references: GB:S79852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 FRRLHCTRNYIH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 FREHCTRNYIH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 FRRLHCTRNYIH 180
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glucagon receptor precursor - human class Homo sapiens (man)  
Claste: 27-un-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999  
Claste: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999  
Clacession: JC2041  
RimacNeil, D.J.; Occi, J.L.; Hey, P.J.; Strader, C.D.; Graziano, M.P. Biochem Biophys. Res. Commun. 138, 328-334, 1994  
A;Title: Cloning and expression of a human glucagon receptor. A;Reference number: JC2041; MUID:94121651  
A;Accession: JC2041  
A;Accession: JC2041  
A;Molecule type: mRNA  
A;Residues: 1-477  
A;Accession: JC2041  
A;Molecule type: mRNA  
A;Residues: 1-477  
A;Accession: JC3041; MUID:94121651  
A;Accession: JC3041  
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NID:g1030050; PIDN:CAA57426.1; PID:g1030051
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100.0%; Pred. No. 0.093;
ive 0; Mismatches (
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; Search time 13.32 Seconds (without alignments) 1391.308 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             93435 segs, 34255486 residues
                                                                                                                             September 21, 2001, 17:09:57
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                                                                                      - protein search, using sw model
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Word size :

Searched:

Minimum DB Maximum DB

Database :

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P49190 homo sapien	P70555 rattus norv	P25107 didelphis m	P47872 homo sapien	P23811 rattus norv	P50133 sus scrofa	P41593 mus musculu	P25961 rattus norv	Q03431 homo sapien	_	Q90308 carassius a	P43219 rattus norv	P32241 homo sapien	Q28992 sus scrofa	P30083 rattus norv	P43218 mesocricetu	P48546 homo sapien	P47871 homo sapien	Q920w0 rattus norv	095838 homo sapien
SUMMARIES	Œ	PTR2_HUMAN	PTH2_RAT	PTRR_DIDMA	SCRC_HUMAN	SCRC_RAT	PTRR_PIG	PTRR_MOUSE	PTRR_RAT	PTRR_HUMAN	SCRC_RABIT	VIPR_CARAU	GIPR_RAT	VIPR_HUMAN	VIPR_PIG	VIPR_RAT	GIPR_MESAU	GIPR_HUMAN	GLR_HUMAN	GLP2_RAT	GLP2_HUMAN
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dР	Query Match	67.1	6.1	4.6	3.5	3.5	3.3	3.3	3.3	3.3	3.0	3.0	2.4	2.4	2.4	2.4	2.4	2.5	1.8	1.8	1.8
	Score	363	33	25	19	19	18	18	18	18	16	16	13	13	13	13	13	12	10	10	10
	Result No.	-	7	М	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20

(Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR). 550 AA PRT; STANDARD; PTR2_HUMAN P49190; 01-FEB-1996 (01-FEB-1996 (01-OCT-2000 (PARATHYROID H PTR2_HUMAN RESULT E H H H H H

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@isb-sib.ch).
                                                                                                                                                                                                                                                       MEDLINE-97079671; PubMed-8921382;
Usdin T.B., Modi W., Bonner T.I.;
"Assignment of the human PTH2 receptor gene (PTHR2) to chromosome 2q33
by fluorescence in situ hybridization.";
Genomics 37:140-141(1996).
                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                  Usdin T.B., Gruber C., Bonner T.I.;
"Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTHZ receptor.";
J. Biol. Chem. 270:15455-15458(1995).
                                                                                                                                                                                                                                                                                                                                                                              ADENYLYL CYCLASE.
--- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.
ALSO EXPRESSED IN THE TESTIS.
--- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS0650; G_ROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARATHYROID HORMONE RECEPTOR.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                               SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                        SEQUENCE OF 26-40 AND 306-550 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U25128; AAC50157.1; -.
EMBL; U47129; AAC405796.1; -.
EMBL; U47129; AAC50767.1; -.
EMBL; U47125; AAC50767.1; JOINED.
EMBL; U47126; AAC50767.1; JOINED.
EMBL; U47127; AAC50767.1; JOINED.
EMBL; U47128; AAC50767.1; JOINED.
GCRDb; GCR_2003; -.
                                                                                                                                 MEDLINE=95318121; PubMed=7797535;
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Pfam; PF00002; 7tm_2; 1.
PRINTS; PR00249; GPCRSECRETIN.
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121
550 AA;
                                                                NCBI_TaxID=9606
                                                                                                                 TISSUE-Brain;
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European Bioinformatics Institute.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDGOCTIOLOGY 137:4285-4297(1996).

-I- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDICATED BY G PROTEINS WHICH ACTIVATE ADENTLYIL CYCLASE. PTHR2 MAY BE RESPONSIBLE FOR PH EFFECTS IN A NUMBER OF PHYSIOLOGICAL SYSTEMS. IT MAY PLAY A SIGNIFICANT ROLE IN PANCREATIC FUNCTION. PTHR2 PRESENCE IN NEURONS INDICATES THAT IT MAY FUNCTION AS A NEUROTRANSMITTER RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96426194; PubMed=8828488;
Usdin T.B., Bonner T.I., Harta G., Mezey E.;
"Distribution of parathyroid hormone-2 receptor messenger ribonucleic
                                                                                                                                                                                                                                                   243
                                                                                                                         123
                                                                                                                                           FPEWDGLICWPRGTVGKISAVPCPPYINDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYS 123
                                                                                                                                                                                        DCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHL 183
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                Gaps
                                                                             4 LGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGEGNC 63
                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN, ARTERIAL AND CARDIAC ENDOTHELIUM. FOUND AS WELL IN SPERM, IN THE HEAD OF THE EPIDIDYMIS. LOWER EXPRESSION IS FOUND IN VASCULAR SMOOTH MUSCLE, EXOCRINE PANCREAS, TESTIS AND PLACENTA.
-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                              LGASLHVWGWLMLGSCLLARAQLDSDGT1T1EEQ1VLVLKAKVOCELN1TAOLOEGEGNC
                                                                                                                         FPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANYS
                                                                                                                                                                                                      FVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAVVMF
                                                                                                                                                                                                                                                                     IYFLATNYYWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLAD
                                                                                                                                                                                                                                                                                                                                  ARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRKLAK
                                                                                                                                                                                                                                                                                                                                                                                                STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
 Length 550;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV 7-1997 (Rel. 39, Last annotation update)
PARRATHYROLD HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 AA
                               0; Mismatches
Score 363;
Pred. No. 0;
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67.1%;
99.8%;
                               Conservative
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              Similarity
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                               463;
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P70555;
Query Match
Best Local 9
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                               Matches
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use by non-profit institutions as long as its content is in on way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                    7 (POTENTIAL).
CYDODIASHIC (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
W., 2825AE4040313527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Didelphis marsupialis virginiana (North American opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
                                                                          InterPro; IPR000832; -.
Pfam; PF00002; 7tm_2; 1.
PRINTS; PR00249; GPCRECRETIN.
PROSITE; PS00669; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS500560; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schipani
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THIS
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                                                                                                                                                           PARATHYROID HORMONE RECEPTOR
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                                                                                                                                                                                                                                         4 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            146 YTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                   148 YTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH 180
                                                                                                                                                                                                                                                                                                                                                                                             Score 33;
                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-NOV-1995 (Rel. 32, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                61800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRECURSOR (PTH/PTHR RECEPTOR)
                                                         EMBL; U55836; AAC52849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9267;
                                                                                                                                                           381
392
415
51
106
116
                                                                  GCRDb; GCR_1
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P25107;
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CARBOHYD
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TISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                PARATHYROID HORMONE/PARATHYROID HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                        SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                              CTIVELACULA.

6 (POTENTIAL).

EXPRACELULIAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

"TWEEN (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens (Human).
Wasaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                       PRINTS; PR00249; GPCKSECRETIN.
PRINTS; PR00293; PTRHORMONER.
PROSITE; PR00593; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00277; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
STANDING TECEPLOT; Transmembrane; Glycoprotein; Signal.
SIGNAL POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 1; Length 585;
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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34900384CD6DF477 CRC64;
                                                                                                                                                                                                                                                                                            RELATED PEPTIDE RECEPTOR
                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.8e-17;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCRC_HUMAN STANDARD; PRT; 440 AA. P47872; 013213; 012961; 01-FEB-1996 (Rel. 33, Created) 10-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) SECRETIN RECEPTOR PRECURSOR (SCT-R).
                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 GYFRRLHCTRNYIHMHLFVSFMLRA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MΚ
                                                                                                                                            EMBL; M74445; AAA30979.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65963
                                                                                                                                                                        InterPro; __PR000832; -.
InterPro; IPR002170; -.
Pfam; PF00002; 7tm_2; 1.
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                                                                                                                                                        PIR; A39286; A392
GCRDb; GCR_0204;
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337
4404
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4435
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1163
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                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lung;
MEDLINE-95214632; PubMed=7700244;
MEDLINE-95214632; PubMed=7700244;
Patel D.R., Kong Y., Sreedharan S.P.;
"Molecular cloning and expression of a human secretin receptor.";
Mol. Pharmacol. 47:467-473(1995).
-: FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROFEINS WHICH ACTIVATE ADENYLYL
                                                                           Jiang S., Ulrich C.D.; {\tt "Molecular} cloning and functional expression of a human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00550; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                     a human
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECRETIN RECEPTOR. EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                "Molecular cloning and functional characterization
                                                                                                                                                                                                                                                                                                                          secretin receptor.";
Biochem. Biophys. Res. Commun. 212:204-211(1995).
                                                                                                                                                 Biochem. Biophys. Res. Commun. 207:883-890(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (POTENTIAL)
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SEQUENCE FROM N.A.
TISSUE=Pancreas;
MEDLINE=95169147; PubMed=7864894;
                                                                                                                                                                                                                                                 MEDLINE=95336443; PubMed=7612008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U20178; AAC50106.1; --
EMBL; U13881; AAA64949.1; --
GCRDb; GCR_1995; --
GCRDb; GCR_2016; --
GCRDb; GCR_2016; --
GCRDb; GCR_2018; --
INTERPO; IPR00031; --
INTERPO; IPR00031; --
FTAML; PR000249; GCREEKEFIN.
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362
362
392
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440
72
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                            secretin receptor.
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PTRR_PIG
P50133;
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                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28BO J. 10:1635-1641(1991).
-1- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRU02144; ...
PREMINES PRO0002; 7tm_2; 1.
PRINTS; PRO0490; SECRETIN.
PRINTS; PRO0490; SECRETINR.
PROSITE; PSO0649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PSO0650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PSO027; G_PROTEIN_RECEP_F2_3; 1.
C_PROTEIN_RECEP_F2_3; 1.
22 POTENTIAL.
23 449 SECRETIN RECEPTOR.
23 449 SECRETIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular cloning and expression of a cDNA encoding the secretin
     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
Nagata S.;
                      (POTENTIAL)
                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                 DB 1; Length 440;
2e-11;
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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                    0; Indels
N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
G -> A (IN REF. 1).
A -> P (IN REF. 2).
I -> F (IN REF. 3).
E -> Q (IN REF. 3).
G -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                20, Created)
20, Last sequence update)
25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 449 AA
                                                                                                                                                                               3.5%; Score 19; DB 100.0%; Pred. No. 2e-tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Last sequence of the contraction of the contract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-91266890; Pubmed-1646711;
                                                                                                                             ΨM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X59132; CAA41849.1; -. PIR; S16319; S16319.
                                                                                                                                                                                                                                                     169 FRRLHCTRNYIHMHLFVSF 187
                                                                                                                                                                                                                                                                           167 FRRLHCTRNYIHMHLEVSF 185
                                                                                                                             50206
                                                                                                                                                                             Ouery Match 3.59
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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InterPro; IPR000832; -.
InterPro; IPR002144; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
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2291
124
210
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333
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4449
143
167
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291
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210
308
333
377
440 AA;
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01-NOV-1991 (Rel.
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EMBO J. 1(
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TRANSMEM
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SEQUENCE
                    CARBOHYD
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SCRC_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                 5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLOLAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE=96305358; PubMed=8688470;
Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
Black E.C., Halung H.M.;
"Structure and functional expression of a complementary DNA for porcine parathyroid hormone/parathyroid hormone-related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                    4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 AA
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3 (POTENTIAL)
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InterPro; IPR000832; -.
InterPro; IPR002170; -.
Pfam; PF00002; 7tm_2; 1.
PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00393; PTRHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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240
254
2276
2276
3317
343
343
343
344
346
100
100
1106
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PARATHYROID HORMONE/PARATHYROID HORMONE-
  CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                   SYSTEM.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00393; PTRHORMONER.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS0027; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLOLAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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GA -> VS (IN REF. 2).
F7876F8D388BDDFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELATED PEPTIDE RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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2.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                      EMBL; L34611; AAA40011.1; -.
EMBL; L34608; AAA40011.1; JOINED.
EMBL; L34607; AAA40011.1; JOINED.
EMBL; L34609; AAA40011.1; JOINED.
EMBL; L34610; AAA40011.1; JOINED.
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ilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66313 MW;
                                                                                                                                                                           EMBL; X78936; CAA55536.1; -.
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GCRDb; GCR_1614; -.
MGD; MGI:97801; Pthr.
InterPro; IPR000832; -.
InterPro; IPR002170; -.
Pfam; PF00002; 7tm_2; 1.
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591
151
161
166
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500
591 AA;
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Best Local Similarity
Matches 18; Conserv
                SYSTEN
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TRANSMEM
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TRANSMEM
DOMAIN
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                                                                 PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTRR_MOUSE STANDARD; PRT; 591 AA.
P41593; Q62119;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCuaig K.A., Clarke J.C., White J.H.;

"Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyroid hormone-related peptide receptor.";

Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).

-i- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS' RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
G_PROTEIN_RECEP_F2_1; 1.
G_PROTEIN_RECEP_F2_2; 1.
G_PROTEIN_RECEP_F2_3; 1.
receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C3H/HEHA;
MEDLINE-95034305; PubMed-7524627;
MEDLINE-95034305; PubMed-7524627;
Marperlan M., van Dijk T.B., Hoeljmakers T., Cremers F.,
Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
"Expression pattern of parathyroid hormone-parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes.";
                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                               Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                  2 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                       CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
                                                                                                                                                                                                                                                                                                                                                                                            3.3%; Score 18; DB 1; Le
100.0%; Pred. No. 2.8e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                     7 (POTENTIAL)
                                                                                                            1 (POTENTIAL)
                                                                                                                                                                                                                                              (POTENTIAL)
                                                      POTENTIAL.
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MEDLINE-94255468; PubMed-8197183;
                                                                                                                                                                                                                                                                                                                                                      MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRECURSOR (PTH/PTHR RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 YFLATNYYWILVEGLYLH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mech. Dev. 47:29-42(1994).
                                                                                                                                                                                                                                                                                                                                                      65682
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                                                                                           184
208
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nes 18; Conserv
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            PS00650;
PS50227;
                                       G-protein coupled
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PROSITE;
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CARBOHYD
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  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,
Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;
"Cloning of a parathyroid hormone/parathyroid hormone-related peptide
receptor (PTHR) cDNA from a rat osteosarcoma (UMR 106) cell line:
chromosomal assignment of the gene in the human, mouse, and rat
                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                              TISSUE-Bone;
MEDINE-9212903; PubMed-1313566;
Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
Kronenberg H.W., Segre G.V.,
Expression cloning of a common receptor for parathyroid hormone and
parathyroid hormone-related peptide from rat osteoblast-like cells: a
single receptor stimulates intracellular accumulation of both cAMP
and inositol trisphosphates and increases intracellular free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 20:20-26(1994).

-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADBIVITY CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (POTENTIAL)
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                                                                PRECURSOR (PTH/PTHR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M77184; AAA41811.1; -. EMBL; L19475; AAA68098.1; -.
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10116;
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MEDLINE=93238641; PubMed=8386612;
Schipani E., Karga H., Karapia A.C., Potts J.T. Jr., Kronenberg H.M.,
Abou Samra A.-B., Segre G.V., Jueppner H.;
"Identical complementary deoxyribonucleic acids encode a human renal
and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
Endocrinology 132:2157-2165(1993).
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                  CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MM; 21944F3051B9E9C1 CRC64;
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STRUCTURE BY NMR OF 168-198.
MEDLINE-98409426; PubMed-9737850;
Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARATHYROLD HORMONE/PARATHYROLD HORMONE-RELATED PEPTIDE RECEPTOR
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                                                                                                                                                                                                                                                                                                                              Score 18; DB 1; Length 591 Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Endocrinol. Metab. 80:1611-1621(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AA.
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  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93387403; PubMed=8397094;
                                                                                                                                                                                                                                                                                                                              3.3.,
100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 YFLATNYYWILVEGLYLH 307
                                                                                                                                                                                                                                                                                                                              Query Match 3.3 Best Local Similarity 100. Matches 18; Conservative
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382
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SCRC_RABIT
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or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHONDRODYSPLASIA, A SEVERE SKELETAL DISPLASYIA.

CHONDRODYSPLASIA, A SEVERE SKELETAL DISPLASYIA.

DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF WURK-JANSEN TYPE OF

METAPHYSEAL CHONDRODYSPLASIA, A SEVERE SKELETAL DISPLASYIA. IT IS

A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA

AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
                                                                                                                                                                                                                                                                                                                           Juppner H.;
"Constitutive activation of the cyclic adenosine 3',5'-monophosphate signaling pathway by parathyroid hormone (PTH)/PTH-related peptide chondrodysplasia ";
                                                                                                                                                                                                                                                                                                                                                                                               MOI. Endoctinol. 11:851-858(1997).
-!-FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES: MOST ABUNDANT IN KIDNEY, BONE AND LIVER.
-!- DISEASE: DEFECTS IN PTHR1 ARE THE CAUSE OF BLOMSTRAND TYPE OF
                                                                                                                                                                                                                                                                                                                 Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                   VARIANT MURK-JANSEN ARG-223.
MEDLINE-95215874; PubMed-7701349;
Schipanl E., Kruse K., Juppner H.;
A constitutively active mutant PTH-PTHrP receptor in Jansen-type metaphyseal chondrodysplasia.";
Science 268:98-100(1995).
                                                                                                                                                  VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
MEDLINE-96366745; PubMed-8703170;
Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
Kooh S.W., Cole W.G., Juppner H.;
"Constitutively activated receptors for parathyroid hormone and
parathyroid hormone-related peptide in Jansen's metaphyseal
Binding domain of human parathyroid hormone receptor: from
                                                                                                                                                                                                                                                       New Engl. J. Med. 335:708-714(1996).
                                                                                                                                                                                                                                                                                     MUTAGENESIS OF ARG-223 AND PRO-410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U22401, AAB60657.1, JOINED. EMBL, U22402, AAB60657.1, JOINED. EMBL, U22403, AAB60657.1, JOINED. EMBL, U22404, AAB60657.1, JOINED. EMBL, U22405, AAB60657.1, JOINED. EMBL, U22407, AAB60657.1, JOINED. EMBL, U22407, AAB60657.1, JOINED. EMBL, U22407, AAB60657.1, JOINED.
              conformation to function.";
Biochemistry 37:12737-12743(1998).
                                                                                                                                                                                                                                                                                                  MEDLINE-97322091; Pubmed-9178745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L04308; AAA36525.1; -. EMBL; X68596; CAA48589.1; -.
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U17418; AAAS6774.1;
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GCRDb; GCR_0205; -.
GCRDb; GCR_0647; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; U17418; AAA5677
S29610; S29610.
A49191; A49191.
                                                                                                                                                                                                                                          chondrodysplasia.";
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PARATHYROID HORMONE/PARATHYROID HORMONE
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H -> R (IN MURK JANSEN; CONSTITUTIVELY
ACTIVATED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FIId=VAR_003582,
T -> P (IN MURK JANSEN; CONSITIUTIVELY
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
MIM; 168468; -.
MIM; 156400; -.
MIM; 156400; -.
MIM; 215045; -.
InterPro; 1PR000832; -.
InterPro; 1PR00170; -.
PRIM; PR000249; GPCESECRETIN.
PRINTS; PR00349; PTRHORMONER.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00550; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00557; G_PROTEIN_RECEP_F2_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
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MEDILINE-98366112; Pubmed-9700755;
Svoboda M., Tastenoy M., de Neef P., Delporte C., Waelbroeck M.,
Robberecht P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (PC
N-LINKED (GLCNAC...) (PC
N-LINKED (GLCNAC...) (PC
N-LINKED (GLCNAC...) (PC
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-> C (IN REF. 2).
DA1400640A6C7F2B CRC64;
                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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100.08; Pre-
                                                                                                                                                                                             Disease mutation; 3D-structure.
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Best Local Similarity 100.
Matches 18; Conservative
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593 AA;
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GCRDb; GCRDb;

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Cypriniformes; Cyprinidae; Cyprininae; Carassius
                 NCBI_TaxID=7957;
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TRANSMEM
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GIPR_RAT
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                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Molecular cloning and in vitro properties of the recombinant rabbit
                                                         THIS
                                                                                                      -1- SUBGELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR).
Carassius auratus (Goldish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor; Transmembrane; Glycoprotein; Signal.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                      -1- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 445; 2.5e-08;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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SECRETIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000832; -.
InterPro; IPR001771; -.
InterPro; IPR001771; -.
InterPro; IPR001771; -.
InterPro; IPR00244; -.
Pfam; PF00002; 7tm_2; 1.
PRINTS; PR00490; SECRETINN.
PRINTS; PR00490; SECRETINN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS0027; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS0027; G_PROTEIN_RECEP_F2_3; 1.
PROTEIN_RECEP_F2_3; 1.
PROTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50495 MW;
                 secretin receptor.";
Peptides 19:1055-1062(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 FREHCTRNYIHMHLF 178
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Best Local Similarity 100.
Matches 16; Conservative
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SEQUENCE FROM N.A.
MEDLINE=97190233; PubMed=9038250;
MEDLINE=97190233; PubMed=9038250;
Chow B.K.C., Yuen T.T.H., Chan K.W.;
"Molecular evolution of vertebrate VIP receptors and functional characterization of a VIP receptor from goldfish Carassius auratus.";
Gen. Comp. Endocrinol. 105:176-185(1997).
-!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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Pfam; PF00002; 7tm_2; 1.
PRINTS; PR000249; GFORSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00527; G_PROTEIN_RECEP_F2_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (P
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Matches 16; Conservative
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159 FRRLHCTRNYIHM 171

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EMBL;
                                                            VIPR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            -!- SÜBCELLÜLAR LOCATION: INTEGRAL MEMBRANE PROFEIN.
-!- TISSUE SPECIFICITY: PRESENT IN THE PANCREAS AS WELL AS THE GUT,
ADIPOSE TISSUE, HEART, PITUTTARY, AND INNER LAYERS OF THE ARRENAL
CORTEX, WHEREAS IT IS NOT FOUND IN KIDNEY, SPLEEN, OR LIVER. IT IS
ALSO EXPRESSED IN SEVERAL BRAIN REGIONS, INCLUDING THE CEREBRAL
CORTEX, HIPPOCAMPUS, AND OLFACTORY BULB.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE-94062667; PubMed-8243312;
Usdin T.B., Mezey E., Button D.C., Brownstein M.J., Bonner T.I.;
Usdin T.B., Mezey E., Button D.C., Brownstein M.J., Bonner T.I.;
Gastric inhibitory polypeptide receptor, a member of the secretin-
vasoactive intestinal peptide receptor family, is widely distributed
in peripheral organs and the brain.";
Endocrinology 133:2861-2871(1993).
-i- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR0013; -.
InterPro; IPR001749; -.
InterPro; IPR001249; -.
PRIM: PR000249; GPRESERETIN.
PRINTS; PR00129; GPRESERETIN.
PRINTS; PS006649; G-PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00277; G-PROTEIN_RECEP_F2_2; 1.
G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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3 (POTENTIAL).
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5454B0638ABF9A06 CRC64;
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2 (POTENTIAL).
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                           Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52256 MW;
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                norvegicus (Rat).
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186
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69
74
455 AA;
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Best Local Similarity
Matches 13; Conserv
                                                                                         SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10116;
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136
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VIPR_HUMAN STANDARD; PRT; 457 AA.

912.241; 015.811;
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
(PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I., Ogier-Denis E., Laburthe M.; "Human intestinal VIP receptor: cloning and functional expression of two CDNA.encoding proteins with different N-terminal domains."; Biochem. Biophys. Res. Commun. 200:769-776(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modecular cloning and functional characterization of a human liver vascactive intestinal peptide receptor.";

"Molecular cloning and functional characterization of a human liver vascactive intestinal peptide receptor.";

cell. Signal. 6:321-333(1994).

-!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVITY OF THIS RECEPTOR. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRODUCED BY ALTERNATIVE

-!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIVER AND PLACENTA.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLICING.
-!- TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS, RAJI B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY,
                                                                                                                                                                                                                                                                                                                      Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.; "Cloning and functional expression of a human neuroendocrine vascative intestinal peptide receptor."; Blochem. Biophys. Res. Commun. 193:546-553(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING TISSUE=Intestine;
                                                                                                                                (PACAP TYPE II RECEPTOR) (PACAP-R-2)
                                                                                                                                                                                                                                                                                 TISSUE=Intestine;
MEDLINE=93290641; PubMed=8390245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
MEDLINE=95001220; Pubmed=7917790;
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AAB60362.1;
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AAA36805.1;
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CAA53046.1;
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                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=9606;
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U11084;
U11085;
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L13288;
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Gaps

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R InterPro; IPR000832; -.
R InterPro; IPR001771; -.
R Pfam; PF00002; 7tm_2; 1.
R PRINTS; PR001491; VASOACTVEIPR.
R PRINTS; PR001491; VASOACTVEIPR.
R PRINTS; PR001491; VAPIACEP_TOR.
R PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
R PROSITE; PS00550; G_PROTEIN_RECEP_F2_2; 1.
R PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; 1.
R PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; 1.
R PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
R PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
R PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
R PROSITE; PS50227; G_PROT
                                                                                                                RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE (BY SIMILARITY)
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONG TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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1-APR-1993 (Rel. 25, Last sequence update)
01-APR-1997 (Rel. 35, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL)
         SEQUENCE FROM N.A.
Hsiung H.M., Smith D.P., Hyslop P.A., Heiman M.L., Hassan H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                        Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. . .) (P
E166E4D6B3BE1189 CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (P
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
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VIPR_RAT
ID VIPR_RAT
AC P30083;
DT 01-APR-199
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DT 01-APR-199
DT VASOACTIVE
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SEQUENCE
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LLSLRRLGGGWSAVTRLVVAAAGARSRGGGGGGGGG
GGVARRRRLELRAARSLLGSS (IN LONG ISOFORM).
DAAAOCF5BEC4707D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
(PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
(PACAP TYPE II RECEPTOR) (PACAP-R-2).
VIPRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                             InterPro; IPR000832; -.
InterPro; IPR001571; -.
InterPro; IPR001571; -.
InterPro; IPR001571; -.
Prints: PR00249; GFCRSECREIN.
PRINTS: PR00249; GFCRSECREIN.
PRINTS: PR001154; VPIBECEPPO.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS06650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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0; Mismatches
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EMBL; L20295; AAA36802.1; -
PIR; JN0604; JN0604.
GCRDb; GCR_0397; -
GCRDb; GCR_062; -
GCRDb; GCR_0774; -
GCRDb; GCR_0704; -
GCRDb; GCR_1888; -
MIM; 192321; -
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VIPR_PIG
ID VIPR_PIG
Q28992;
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 (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
(PACAP TYPE II RECEPTOR) (PACAP-R-2).
                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN
(MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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PRINTS; PR00491; VASOACTVEIPIN.
PRINTS; PR00491; VASOACTVEIPIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS0050; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-PROTEIN_RECEP_F2_3; 1.
G-PROTEIN_RECEP_F2_3; 1.
G-PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-PROTEIN_RECEP_F2_3; 1.
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N-LINKED
                                                                                                                                                  MEDLINE=92232309; PubMed=1314625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000832; -.
InterPro; IPR001571; -.
InterPro; IPR001771; -.
Pfam; PF00002; 7tm_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCRDb; GCR_0369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
292
459 AA;
                                                                                                                    SEQUENCE FROM N.A. TISSUE-Lung;
                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                           CYCLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                              MEDLINE=95110292: PubMed=7811236, Yasuda K., Inagaki N., Yamada Y., Kubota A., Seino S., Seino Y.; Yasuda K., Inagaki N., Yamada Y., Kubota A., Seino S., Seino Y.; "Hamster gastric inhibitory polypeptide receptor expressed in pancreatic islets and clonal insulin-secreting cells: its structure
                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
03-STRIC IMHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: WIDELY INSTRIBUTED INCLUDING PANCREATIC ISLETS, BRAIN AND VARIOUS PERIPHERAL TISSUES.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                       and functional properties.";
Blochem. Biophys. Res. Commun. 205:1556-1562(1994).
-!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROFEINS WHICH ACTIVATE ADENYLYL.
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EXTRACELLULAR (POTENTIAL).
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000832; -.
InterPro; IPR001749; -.
Prim: PF00002; 7tm_2; 1.
PRINTS; PR001249; GPCRSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS0027; G_PROTEIN_RECEP_F2_3; 1.
G_PROTEIN_RECEP_F2_3; 1.
ROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
ROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
ROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
ROSICAL
                     462 AA.
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                                                                                                                                                                     Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D38103; BAA07284.1; -.
                     STANDARD;
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135
135
1158
1166
128
214
233
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290
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GIPR_MESAU
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Gaps

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2.4%; Score 13; DB 1; Length 459; 100.0%; Pred. No. 3.1e-05; Lve 0; Mismatches 0; Indels

100.08;

Best Local Similarity 100. Matches 13; Conservative

Query Match

CYCLASE

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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsequence analysis of a 1.9 Mb region in 19q13.2 between APOE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning, functional expression, and signal transduction of
the GIP-receptor cloned from a human insulinoma.";
FEBS Lett. 373:23-29(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gremlich S., Porret A., Hani E.H., Cherif D., Vionnet N., Froguel P.,
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning, functional expression, and chromosomal localization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDILINE-96121393; PubMed-8575774;
MEDILINE-96121393; PubMed-8575774;
Wamada Y., Hayami T., Nakamura K., Kaisaki P.J., Someya Y.,
Wamada Y., Seino S., Seino Y.;
"Human gastric inhibitory polypeptide receptor: cloning of the gene
(GIPR) and cDNA.";
Genomics 29:773-776(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human pancreatic islet glucose-dependent insulinotropic polypeptide
                                                                                                                                                                                                      GIPR_HUMAN STANDARD; PRT; 466 AA.

945366, 014401;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GASTRAIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96013879; PubMed-7589426;
Volz A., Goke R., Lankat-Buttgereit B., Fehmann H.C., Bode H.P.,
Goke B.;
 N-LINKED (GLCNAC. . .) (POTENTIAL).
             (POTENTIAL)
                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
                                                                DB 1; Length 462; 3.1e-05;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                       Usdin T.B., Gruber C., Modi W., Bonner T.I.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
             N-LINKED (GLCNAC. .) (PO
D7A6204BCB9BB688 CRC64;
                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUE-Pancreas;
MEDLINE-96007224; PubMed-7556958;
                                                               2.4%; Score 13; DB 100.0%; Pred. No. 3.1 ive 0; Mismatches
                          MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diabetes 44:1202-1208(1995).
                         52918
                                                            Query Match 2.4
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                               159 FRELHCTRNYIHM 171
                                                                                                                  169 FRRLHCTRNYIHM 181
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                         462 AA;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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CARBOHYD
CARBOHYD
                         SEQUENCE
                                                                                                                                                                               RESULT 17
GIPR_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseefisb-sib.ch).
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                                                   -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V -> VGRDPAAPALWRRGTAPPLSAIVSOV (IN LONG ISOFORM).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
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Pred. No. 0.00033;
0; Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CA5CF86BA0E32383 CRC64;
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CYTOPLASMIC (POTENTIAL).
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G -> R (IN REF. 2).
MISSING (IN REF. 3).
L -> V (IN REF. 2).
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                                                                                                                                                                                                                                            ; 579852; AAB35419.2; -. X81832; CAA57426.1; -. D49559; BAA08503.1; -. D49555; BAA08503.1; JOINED.; D49557; BAA08503.1; JOINED.; D49558; BAA08503.1; JOINED.
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100.0%; Pre
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PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR01129; GIPRECEPTOR.
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\frac{117}{337}
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InterPro; IPR001749;
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GCRDb, GCR_1157; --
GCRDb; GCR_1955; --
GCRDb; GCR_1987; --
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466 AA;
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Best Local Similarity
                                    SPLICING
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DOMAIN
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EMBL; AF105368; AAD16896.1; -.
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                                                                                                                                                                                                                                                                                                                                                       [2] SEQUENCE FROM N.A. MEDILINE-9419299; PubMed-8144028; Kramer J.M., Whitmore T.E., Lok S., Kuijper J.L., Jelinek L.J., Kramer J.M., Whitmore T.E., Spreecher C.A., Mathewes S., Grant F.J., Biggs S.H., Rosenberg G.B.; "The human glucagon receptor encoding gene: structure, cDNA sequence and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DISEASE: IT IS A CANDIDATE FOR CERTAIN DEFECTS IN NON-INSULIN-
DEPENDENT DIABETES MELLITUS (NIDDM): THE VARIANT IN POSITION 40
(SER) IS FOUND IN SOME NIDDM PATIENTS, BUT ALSO IN NONDIABETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection Provided: 1.

PRINTS: PRO0024; Thm.2: 1.

PRINTS: PR000249; GPCRSECRETIN.

PROSITE: PS00649; G_PROTEIN. RECEP_F2_1; 1.

PROSITE: PS00609; G_PROTEIN. RECEP_F2_2; 1.

PROSITE: PS0027; G_PROTEIN. RECEP_F2_3; 1.

G_Protein coupled receptor; Transmembrane; Glycoprotein; Signal; SIGNAL.

SIGNAL.
                                                                                                                                                                                                           Macneil D.J., Occi J.L., Hey P.J., Strader C.D., Graziano M.P.; "Cloning and expression of a human glucagon receptor."; Biochem. Biophys. Res. Commun. 198:328-334(1994).
                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
12-UL-1998 (Rel. 36, Last annotation update)
GLUCAGON RECEPTOR PRECURSOR (GL-R).
                                          477 AA
                                                                                                                                                                                                MEDLINE-94121651; PubMed-7507321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U03469; AAC52063.1; -. EMBL; L20316; AAA53628.1; -.
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                         Gene 140:203-209(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCRDb; GCR_0772; -. GCRDb; GCR_0881; -.
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                VARIANT SER-40.
                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBJECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 138033;
                                        GLR_HUMAN
P47871;
                               GLR_HUMAN
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MEDINE-99145591; PubMed-9990065;
MEDINE-99145591; PubMed-9990065;
Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
A Demchyshyn L., Yang Z.-H., Kamboj R.K., Chen H., McCallum K.,
A Sumner-Smith M., Drucker D.J., Crivici A.;
T "Prototypic G protein-coupled receptor for the intestinotrophic factor at glucagon-like peptide 2.";
Proc. Natl. Acad. Sci. U.S.A. 96:1569-1574(1999).
T. FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 2. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVITY BELONGSTON INTEGRAL MEMBRANE PROTEIN.

-1- SUBCELLULAR BLOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GLUCAGON-LIKE PEPTIDE 2 RECEPTOR PRECURSOR (GLP-2 RECEPTOR) (GLP-2-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                    CYTOPLASMIC (DOTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
G -> S.
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100.0%; Pred. No. 0.039;
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                     EXTRACELLULAR (POTENTIAL).
                                                                                           EXTRACELLULAR (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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                                                                                                              3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                        CYTOPLASMIC (POTENTIAL).
 GLUCAGON RECEPTOR
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0; Mismatches
                                                                           (POTENTIAL)
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Mammalia; Eutheria; Rodentia;
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Matches 10; Conservative
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243 LVEGLYLHNL 252
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                                                                                                                                                                                                                                                                                                                                                                                                             477 AA;
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(GLP-2R).
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Q9Z0W0;
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GLUCAGON-LIKE PEPTIDE 2 RECEPTOR PRECURSOR (GLP-2 RECEPTOR) (GLP-2-R)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                       Pfam; PF00002; 7tm_2; 1.

PRINTS; PR00249; GPCRSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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CYPOLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
"TANKEN (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
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Pred. No.
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Best Local Similarity 100.
Matches 10; Conservative
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InterPro; IPR000832; -. InterPro; IPR001879; -.
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162
550 AA;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  Interpro; IPR000832; -.
Interpro; IPR001879; -.
Ffam; PF00002; 7tm_2; 1.
Pfam; PF00002; 7tm_2; 1.
PROSITE; PS00649; GPCRECERIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_3; 1.
G_PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
G_PROTEIn coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 ?
POTENTIAL.
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches 10; Conserv
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Search completed: September 21, 2001, 17:13:01 Job time: 184 sec

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Gaps

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Compugen Ltd
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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 protein search, using sw model OM protein September 21, 2001, 17:10:17 Run on:

; Search time 27.75 Seconds (without alignments) 2579.352 Million cell updates/sec

US-09-236-468A-2 541 Perfect score:

1 MAWIGASLHVWGWLMLGSCL.......DDILMEKPSRPMESNPDTEG 541 Sequence:

Scoring table:

425026 segs, 132305027 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

10 Word size : 12

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries

SPTREMBL_16:* Database :

Post-processing: Listing first 1000

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_rodent:* sp_plant:* sp_mammal:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*

SUMMARIES

Description	Q9r1d4 mus musculu	Q9pwb7 brachydanio	Q9prg1 ictalurus p	Q9pvd3 brachydanio	Q9tu31 canis famil	Q9ibg2 gallus gall	Q9yhc6 rana ridibu	Q9rlt8 mus musculu	Q9ji40 mus musculu	Q9pvd2 brachydanio	Q9jiy4 mus musculu	Q9yhc8 rana ridibu
DI	Q9R1D4	Q9PWB7	Q9PRG1	Q9PVD3	Q9TU31	Q91BG2	Ф9хнс6	Q9R1T8	Q9J140	Q9PVD2	Q9JIY4	Q9YHC8
DB	11	13	13	13	9	13	13	11	11	13	11	13
Length	169	575	94	536	595	418	444	459	459	542	48	167
Query B Match Length DB	7.0	5.0	3.7	3.3	3.3	2.4	2.4	2.4	2.4	2.0	1.8	1.8
Score	38	27	20	18	18	13	13.	13	13	11	10	10
Result No.	1	7	Э	4	2	9	7	89	6	10	11	12

ALIGNMENTS

RESULT Q9R1D4

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TISSUENCE FROM N.A.

TISSUENCE FROM N.A.

TISSUENCE FROM N.A.

MEDLINE-93867425; PubMed=10438471;

MEDLINE-93867425; PubMed=10438471;

Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;

A. G protein-coupled receptor from zebrafish is activated by human part thyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of related peptide. Implications for the evolutionary conservation of RT calcium-regulating peptide hormones.";

J. Biol. Chem. 274:23035-23042(1999).

REMBL: AF132082; AAD51908.1;

S. Biol. Chem. 274:23035-23042(1999).

PRAME: PRO0049; G_REMETIN.

PRAME: PRO0049; G_REMETIN.

PROSITE: PS00649; G_PROTEIN_RECEP_F2_1; 1.

PROSITE: PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
"A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of calcium-regulating peptide hormones.";
J. Biol. Chem. 274:23035-23042(1999).
EMBL: AF122083, AAD51909.1;
InterPro; IPR000832:
Pfam; PP00002; 7fm_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 169;
                            01-MAY-2000 (TrEMBLrel: 13, Created)
1-MAY-2000 (TrEMBLrel: 13, Last sequence update)
01-JUN-2000 (TrEMBLrel: 14, Last annotation update)
PARATHYROLD HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
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19674 MW; 748CC8231F1C69EA CRC64;
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0%; Score 38; DB 11; 100.0%; Pred. No. 1.9e-30; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 WIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHD 103
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169 AA.
PRT;
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MEDLINE-99367425; Pubmed-10438471;
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PRELIMINARY;
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169 AA;
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                     NCBI_TaxID=10090;
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NCBI_TaxID=9615;
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Q9TU31;
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MEDLINE-99367425; PubMed-10438471;
Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
Rubin D.A., Hellman Pr., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of calcium-regulating peptide hormones.";
J Blol. Chem. 274:23035-23042(1999).
                                Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HOWINE RECEPTOR THIR.
Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; NCBI_TaxID=7955;
                                                                                                                                                                                                     Ictalurus punctatus (Channel catfish).
Wataryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Siluriformes; Ictaluridae; Ictalurus.
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0
          Length 575;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
                              Indels
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94 AA; 10729 MW; D949182E1D2613EF CRC64;
        DB 13; L
9.8e-19;
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        5.0%; Score 27; DB 100.0%; Pred. No. 9.8 ative 0; Mismatches
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InterPro; IPR001211; -.
PRINTS; PR00249; GPCRSECRETIN.
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        Query Match 5.0
Best Local Similarity 100.
Matches 27; Conservative
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[1]
SEQUENCE FROM N.A.
MEDLINE-99428481; Pubmed=10497171;
Rubin D.A., Jueppner H.,
"Zebrafish Express the Common Parathyroid Hormone-Yearathyroid Hormone-related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is Preferentially Activated by Mammalian and Fugufish Parathyroid Hormone-related Peptide.";
J. Biol. Chem. 274:28185-28190(1999).
EMBL: AF132084; AAF01265.1; -.
HSSP; Q03431; IBL1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 13; Length 536;
Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                  536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66308 MW; 09568ECF38D4D258 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE RECEPTOR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 6; Le
Pred. No. 1.6e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        3.3%; Scor.
100.0%; Pred. No. 1.
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                                                                                                                                                                                              InterPro; IPR000832; -.
InterPro; IPR001879; -.
Pfam; PR00002; 7fm_2; 1.
PRINTS; PR00249; GPCRSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 YFLATNYYWILVEGLYLH 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 GYFRRLHCTRNYIHMHLF 184
                                                                                                                                                                                                                                                                                                               SMART; SM00008; HormR; 1. Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
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444 AA; 50955 MW; 883B25B729314C4C CRC64;
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                                                                                                                                                                                                                                                157 LHCTRNYIHMHLF 169
                                                                                                                                                                                                             172 LHCTRNYIHMHLF 184
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Best Local Similarity
Matches 13; Conserv
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AB022858; 1
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Alexandre D., Anouar Y.;
"A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue distribution characteristics of both VPAC1 and VPAC2 receptors in
                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9YHC6;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASOACTIVE INTESTINAL PEPTIDE/PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE RECEPTOR.
Rana ridibunda (Laughing frog) (Marsh frog).
Rana ridibunda (Laughing frog) (Marsh frog).
Amphibia: Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of chicken VIP receptor cDNA, tissue distribution and chromosomal localization.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB029895; BA495164.1; -.
InterPro; IPR000832; -.
InterPro; IPR001879; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Kansaku N., Shimada K., Saito N., Arakawa K., Suzuki T., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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100.0%; Pred. No. 0.00015;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 418 AA; 48191 MW; 7AE4796ADCB08FF3 CRC64;
                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASCACTIVE INTESTINAL PEPTIDE RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mammals.";
Endocrinology 0:0-0(1999).
EMBL; AF100644; AAD03602.1; -.
InterPro; IPR001872; -.
InterPro; IPR001879; -.
Pfam; PF00202; 7fm_2, 1.
PRINTS; PR00249; G_PROTEIN.RECEP_F2_1;
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 AA
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PRINTS; PR00249; GPCRSCRETIN.
PROSITE; PS00649; GPROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                        · PRT;
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                                                           PRELIMINARY;
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Receptor.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
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                                                                                    Q9IBG2;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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RESULT
Q91BG2
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09YHC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic organization and chromosomal location of the mouse vasoactive intestinal polypeptide 1 (VPAC1) receptor."; Genomics 58:90-93(199).

EMBL, 98022860; BAA81896.1; EMBL, AB022848; BAA81896.1; JOINED.

EMBL, AB022849; BAA81896.1; JOINED.

EMBL, AB022851; BAA81896.1; JOINED.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129SVJ;
MEDLINE=99265976; PubMed=10331949;
Hashimoto H., Nishino A., Shintani N., Hagihara N., Copeland N.G., Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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       Length 444;
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                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 AA; 52094 MW; COC3A9AE1ADF611D CRC64;
                                                                                                                                                                                                                                                                                                  09R178,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE 1 (VPAC1) RECEPTOR.
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09J140;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DB 13; L
0.00016;
thes 0;
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  Query Match 2.4%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
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JOINED.
JOINED.
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BAA81896.1;
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                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN-SWR/J; TISSUE-SMALL INTESTINE;
STRAIN-SWR/J; TISSUE-SMALL INTESTINE;
Bjerknes M., Cheng H.;
"Clonal analysis of the effects of glucagon-like peptide 2 (GLP-2) and keratinocyte growth factor (KGF) on mouse intestinal epithelial progenitors.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI66265; AAFB9584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexandre D., Anouar Y.,; "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue distribution characteristics of both VPAC1 and VPAC2 receptors in
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TEMBLEEL. 16, Last annotation update)
GLUCAGON RECEPTOR (FRAGMENT).
GLUCAGON RECEPTOR (Laughing frog) (Marsh frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana. NCBI_TaxID=8406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 10; DB 11; Length 48; 100.0%; Pred. No. 0.027; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
GLUCAGON-LIKE PEPTIDE 2 RECEPTOR PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5D5B18AAEE3AF4AF CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                   48 AA.
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InterPro; IPR000832; -.
PRIMP: PR0002; 7tm_2; 1.
PRIMPS; PR00249; GPCRECRETIN.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                   PRT;
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48
5811 MW;
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Les 10; Conservative
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236 YWILVEGLYLH 246
                       252 YWILVEGLYLH 262
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167 AA;
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48 AA;
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TISSUE=PITUITARY;
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"Zebrafish Express the Common Parathyroid Hormone-/Parathyroid Hormone-related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is Preferentially Activated by Mammalian and Fugufish Parathyroid Hormone-related Peptide.";
J. Blol. Chem. 274:28185-28190(1999).
EMBL; AF132085; AAF01266.2;
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                                                                                                                                                                                                  Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;
"Cloning and Fine Mapping of the Vasoactive Intestinal Peptide
Receptor I (VPACI): A Comparative Analysis of Human, Rat and Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE-RELATED PROTEIN RECEPTOR PTH3R.
Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Abrafish) (Zebra danio).
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF266282; AAF77053.1; -.
Interpro; IPR001893; -.
Pfam; PF00002; 7tm_2; 1.
PROMISE, PR00202; 7tm_2; 1.
PROMISE, PR00649; GPRESERETIN.
PROSITE; PS00669; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 AA; 52095 MW; 9D1ADFB8567D4D7F CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update) VASOACTIVE INTESTINAL PEPTIDE RECEPTOR TYPE 1.
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PRINTS; PR00249; GPCRSECRETIN.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
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MEDLINE-99428481; Pubmed-10497171;
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Matches 13; Conservative
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InterPro; IPR001879; -
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                                                          Mus musculus (Mouse)
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Query Match 1.8%; Score 10; DB 13; Length 167; Best Local Similarity 100.0%; Pred. No. 0.081; Matches 10; Conservative 0; Mismatches 0; Indels
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Search completed: September 21, 2001, 17:13:34 Job time: 197 sec

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61 GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
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                                                                                                                                                                                                                                                                           APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HLTDG74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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E: Stewart & Olstein
6 Becker Farm Road
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US-08-086-631-18
US-08-45-930-18
PCT-US3-08174-118
US-08-845-546-10
US-08-845-956-25
US-08-452-930-25
PCT-US3-08174-25
US-08-845-546-12
US-08-845-546-12
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                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                     STAIL.
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
TOTAL TYPE: TEM PS/2
TOTAL TYPE: TEM PS/2
                                                                                                                                                                                                     Sequence 2, Application US/08468011A Patent No. 6030804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
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INFORMATION FOR SEQ ID NO: 2:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, 1
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Best Local Similarity
Matches 541; Conserva
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STREET: 6
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                                                                                  ; Search time 14.41 Seconds
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Sequence 23,
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08 468-011A-11

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US-08 468-011A-25

US-08 468-011A-26

US-08 468-011A-26

US-08 468-011A-27

US-08 468-011A-21

US-08 468-249A-19

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US-08-468-011A-17
US-08-453-956-18
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                                                                                 September 21, 2001, 17:08:12
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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                                                                                                                                    LADARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK
                                                                                                                                                                                                     QAEVKKMMSRWNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSQVAAAHAWCLSLAKLPR
                                                                                                                                                                                                                                                                                                                                        481 SPADSLTATSLYLAMSGVTQSRTASHTLSTRSNKEDSGRQRDDILMEKPSRPMESNPDTE
                                                  MHLFVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SOPPE, Daniel R
APPLICANT: Y1, Li
APPLICANT: Rosen, Craig A
APPLICANT: Roben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07068-1739
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07085
FILING DATE: 05-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 325800-393
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEBEAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9507085 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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amino acid
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CITY: Roseland
STATE: NJ
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                                                                                                                                                                          NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILLIGYFRRLHCTRNYIH 180
                                                                                                                                                                                         MHLEVSFMLRATSIFVKDRVVHAHIGVKELESLIMQDDPQNSIEATSVDKSQYIGCKIAV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
                               Gaps
                                                                          1 MAWLGASLHVWGWLMLGSCLLARAQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 60
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                               Indels
 Length
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Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Soppet, Daniel R
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone:
TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
   .,
   DB
100.0%; Score 541; D
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08468011A Patent No. 6030804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6 Becker Farm Road
CITY: Roseland
                               Matches 541; Conservative
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07068-1739
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274 KYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF 333
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                                                                                                                                       1 EGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW 60
                                                                                                                                                                                                                                                                                                                         APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: G-Protein Parathyroid G-Protein NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 60; DB 3; Length 60; 100.0%; Pred. No. 2.6e-49; live 0; Mismatches 0; Indels
                        Score 60; DB 3; Length 60;
Pred. No. 2.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNAGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELEPHONE: 201-994-1700
               11.1%; Score 100.0%; Pred. No. 2.00.0%; Pred. No. 2.00.00.00; Mismatches
                                                                                                                                                                                                                                                            Sequence 15, Application US/08468011A Patent No. 6030804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Y1, Li
APPLICANT: Rosen, Craig A
APPLICANT: Roben, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TENGTH: 60 amino acids
                                             Best Local Similarity 100.0
Matches 60; Conservative
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Best Local Similarity 100.
Matches 60; Conservative
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MOLECULE TYPE: protein
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GY: linear
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                                                                                                                                                                                                                    RESULT 5
US-08-468-011A-15
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STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-468-011A-15
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                        Query Match
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Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Yi, Li
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 11.1%; Score 60; DB 3; Length 60; Best Local Similarity 100.0%; Pred. No. 2.6e-49; Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                     NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325800-458 (PF201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                  APPLICATION NUMBER: US/08/468,011A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION UNDRABER: 33,073
REFERENCE/COCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                 TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 60 amino acids
                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-468-011A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSE: Carella,
                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6030034
GENERAL INFORMATION:
APPLICANT: Yi, Li
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HIPG74
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                                                                                                                                                                                                                                                                                                                                                                                           Length 59;
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ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 3; Le
Pred. No. 2.2e-48;
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
8e-28;
                                                      NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.9%; Score 59; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 07066-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING ATTE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 37; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-468-011A-25
; Sequence 25, Application US/08468011A
; Patent No. 6030804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 25:
                             ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                  TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 amino acids
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                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-468-011A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sopper, Daniel R
APPLICANT: Y1, Li
APPLICANT: Nosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HLTDG74
NUMBER OF SQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
G-Protein Parathyroid Hormone receptor HLTDG74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Carella, Byrne, Bain, Gilfillan, Cecchi,
E: Stewart & Olstein
6 Becker Farm Road
    TITLE OF INVENTION: G-Protein Parathyroid Hormone rec
TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 28
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Grealla, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 3; LA
Pred. No. 2.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325800-458 (PF201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.1%; Score 60; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 60; Conservative 0; Mismatches
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/GENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-994-1740
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/08468011A Patent No. 6030804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 07068-1739
COMUTER READALE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                    STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Stews
STREET: 6 Becker
CITY: Roseland
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-468-011A-19
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08468249A Patent No. 5886148 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 GYFRILHCTRNYIHMHLFVSFMLRA 191
                                                                                                                  ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 GYFRRLHCTRNYIHMHLEVSFMLRA 55
                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20 SEQUENCE CHARACTERISTICS: FRUGH: 60 amin a cids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.6
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 CORRESPONDENCE ADDRESS:
                                                                       Roseland
                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                       CITY: Rose
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOST. STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-08-468-249A-18
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                                                                                                           COUNTRY:
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   Gaps
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                                                                                                                                                        Sequence 13, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soper, Daniel R
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: G-Protein Parathyroid CORRESPONDENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor TITLE OF INVENTION: HIDG74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 50;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Le. 1e-27;
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NAME: MULLINS, J.G.
RECISTRATION NUMBER: 33.073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVL 370
                                                    1 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LNTVRVLATKIWETNAVGHDTRKOYRKLAKSTLVLVL 37
                                   24 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.8%; Score 37; DB Best Local Similarity 100.0%; Pred. No. le-Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-468 011A-20
Sequence 20, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-468-011A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                   Roseland
                                                                                                                           RESULT 9
US-08-468-011A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: F
STATE:
 Matches
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Gaps
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TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Ush
ZIP: 02110-2804
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
TITING DATE: 06-UNN-1995
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTONNEY AGENT INFORMATION:
NAME: MULLING, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 25; DB 3; Le
100.0%; Pred. No. 2.5e-16;
Live 0; Mismatches 0;
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Gaps

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Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: ECOMBUNANT DNA VECTORS ENCODING SAME NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 585;
                                                                                              Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRIL 22313
ZIP: 22313
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATEMIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
TITING DATE: 25-OCT-1993
                                                                                                 DB 1; Le
. 1.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.6%; Score 25; DB 2; Le
100.0%; Pred. No. 1.9e-15;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
LOCATION: 1.585
COTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125
                                                                                            4.6%; Score 25; DB 100.0%; Pred. No. 1.9 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION 973

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-UNN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UNN-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000324-010
                                                                                                                                                                                    167 GYFRRLHCTRNYIHMHLFVSFMLRA 191
                                                                                                                                                                                                              207 GYFRRLHCTRNYIHMHLFVSFMLRA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 GYFRRLHCTRNYIHMHLFVSFMLRA 191
         Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Swiss, Gerald F.
REGLSTRATTON UNDRER: 30,113
REFERENCE/DOCKET UNDRER: 0003
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 125:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 699 Prince Street
                                                                                              Query Match
Best Local Similarity 100.C
Matches 25; Conservative
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Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                   US-08-142-551B-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
         ; ORGANISM:
US-08-142-439A-6
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STREET: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201

COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PC POSS/MS-TOS
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           ;
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APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
                                                                                                                                                                                                                                                                                                                                                           Query Match 4.6%; Score 25; DB 2; Length 515; Best Local Similarity 100.0%; Pred. No. 1.7e-15; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00697
FILING APPLICATION NUMBER: PCT/EP93/00697
FILING APPLICATION NUMBER: 33-MAR-93
ATTORNEY/AGENT INFORMATION:

NAME: HATTINGCON James J.

REGISTRATION NUMBER: 38,711
REFERENCE/OCKET NUMBER: 3756.204-US
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0123
INFORMATION FOR SEQ ID NO: 6:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFRENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 GYFRRLHCTRNYIHMHLEVSFMLRA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 GYFRRLHCTRNYIHMHLFVSFMLRA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08142439A Patent No. 5670360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
MODECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                            TOPOLOGY: linear: MOLECULE TYPE: protein US-08-468-249A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NATI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-142-439A-6
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Sequence 21, Application US/08468011A
Fatent No. 6030804
GENERAL INFORMATION:
APPLICANT: Y1, Li
APPLICANT: Y2, Li
APPLICANT: Ruben, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stewart & Olstein
STREET: Roseland
CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 585;
       PARATHYROID HORMONE RECEPTOR AND DNA
                                                                                                                                                                                      COUNTEY. USA
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUW TYEE: FIDEPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/4475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FRASET, JAINS K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INDERR: 00786/071003
TELECOMMUNICATION INDERR: 100786/071003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6%; Score 25; DB 2; Le
100.0%; Pred. No. 1.9e-15;
Live 0; Mismatches 0;
TITLE OF INVENTION: PARATHYROID HOR TITLE OF INVENTION: ENCODING SAME NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GYFRRLHCTRNYIHMHLFVSFMLRA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 GYFRLHCTRNYIHMHLFVSFMLRA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 070bollow
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.C
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                 Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-468-249A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-468-011A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: No. 58467470 No. 5846747disk of No. 5846747th America, Inc. STREET: 405 Lexington Avenue, Suite 6400 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                  Bernard Receptor for the Glucagon-Like-Peptide-1 (GLP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.9e-15;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
4.6%; Score 25; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.9e-1!
Matches 25; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHASALTATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439
FILING DATE: 24 NOV-93
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
APPLICATION NUMBER: 38,71
REGISTRATION NUMBER: 38,71
REGISTRATION NUMBER: 38,71
REGISTRATION NUMBER: 38,71
REGISTRATION NUMBER: 38,71
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FELEFAR: 212 867 0123
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: S85 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/869,477 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence 19, Application US/08468249A; Sequence 10, Application US/08468249A; Patent No. 5886148; GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
  207 GYFRRLHCTRNYIHMHLEVSFMLRA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 GYFRELHCTRNYIHMHLFVSFMERA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GYFRRLHCTRNYIHMHLFVSFMLRA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Didelphis virginiana
                                                                                                                   US-08-869-477-6; Sequence 6, Application US/08869477; Patent No. 5846747
                                                                                                                                                                                                               APPLICANT: Thorens, BerTITLE OF INVENTION: RECTITLE OF INVENTION: (GLNUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Thoren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-869-477-6
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ADDRESSEE: No. 58467470 No. 5846747disk of No. 5846747th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,477
                                                                                                                                                                                                                                                                  Score 19; DB 1; L
Pred. No. 6.8e-10;
                                                                                                                                                                                                                                                                Query Match 3.5%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 6.8 Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S/08/142,439
FILING DATE: 24-NOV-93
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-WAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-WAR-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08869477 Patent No. 5846747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORIGINAL SOURCE:

) ORGANISM: Rattus norvegicus

US-08-869-477-5
                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rattus norvegicus
STRAIN: Sprague-Dawley
US-08-142-439A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Harrington, James J. REGISTRATION NUMBER: 38,711 REFERENCE/DOCKET NUMBER: 37 TELECOMMUNICATION INFORMATION: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                          167 FREHCTRNYIHMHLEVSF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               169 FREHCTRNYIHMHLFVSF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 449 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212 cc. TELEPHONE: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                  linear
                               TOPOLOGY: linea
MOLECULE TYPE: pr
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-08-869-477-5
                                                                                                                                                                                                                                                                                                                                                                                                             q
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Sequence 5, Application US/08142439A

Patent No. 5670360

GENERAL INFORMATION:
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1

TITLE OF INVENTION: (GLP-1)

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSE: No. 56703600 No. 5670360th America, Inc.
STREET: Now York
CITY: Now York
STATE: Now York
COUNTRY: U.S.A.

ZIP: 10174-6201

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%; Score 21; DB 3; Length 21;
100.0%; Pred. No. 5.8e-13;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                    325800-458 (PF201)
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/POCKET NUMBER: 33,073
REFERENCE/POCKET NUMBER: 325800-458 (
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
INFORMATION FOR SEQ ID NO: 21:
SEGUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TTYPE: maino acids
TTYPE: maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24 NOV-93
CLASKIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DX 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/COCKET NUMBER: 38,711
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100.298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 KDRVVHAHIGVKELESLIMQD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KDRVVHAHIGVKELESLIMQD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 449 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.9%
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-468-011A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-142-439A-5
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  PARATHYROID HORMONE RECEPTOR AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Segre, Gino V.
APPLICANT: Konenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Juppner, Harald
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 2; L
Pred. No. 7.7e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,819
SR: 00786/071003
                                                                                                                                                                                                                                                                                                                                                  PELICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-WAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                         NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                         ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/07864475A; Patent No. 5494806; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0076
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 YFLATNYYWILVEGLYLH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 593 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-468-249A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
                                                                                                                                                      STATE: MA
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                                                                                          Gaps
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0
                                     Query Match 3.5%; Score 19; DB 2; Length 449; Best Local Similarity 100.0%; Pred. No. 6.8e-10; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Sequence 20, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN 1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/881,702
FILING DATE: 04-NAY-1991
ATPLICATION NUMBER: US 07/681,702
FILING DATE: 04-NAY-1991
ATPLICATION LOBATE: US 07/681,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.3%; Score 18; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis K. ERGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-468-249A-21
Sequence 21, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Segre et al., Gino V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                      167 FREHCTRNYIHMHEEVSF 185
                                                                                                                             169 FRRLHCTRNYIHMHLFVSF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 YFLATNYYWILVEGLYLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 YFLATNYYWILVEGLYLH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 591 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-468-249A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: USA
02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 225 FCITY: Boston
                                                                                                                                                                                                                                          RESULT 19
US-08-468-249A-20
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Sequence 10, Application US/08468011A

Patent No. 6030804

GENERAL INFORMATION:
APPLICANT: SOPPEL, Daniel R
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HITDG74

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road

CITY: Roseland
                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 60;
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100.0%; Pred. No. 5.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                 Query Match 2.6%; Score 14; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 14; Conservative 0; Mismatches 0;
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM FS.5 INCH DISKETTE
COMPUTER: 1BM FS.5 INCH DISKETTE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                              SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
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  617/542-8906
  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO:
                                                                                                                                     TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-468-249A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-468-011A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 TNYYWILVEGLYLH 262
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                                                                                                                                                                                                                                                                                                                                                                    6 YFLATNYYWILVEG 19
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Best Local Similarity
Matches 14; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                           TYPE: amino acid
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Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segere et al., Gino V.
TITLE OF INVENTION: ENCOING SAME
TITLE OF INVENTION: ENCOING SAME
TUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Score 14; DB 1; Length 19; 100.0%; Pred. No. 2.1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: BOSTON
COUNTRY: WAS
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TENDED COMPATIBLE
COMPUTER: TENDED COMPATIBLE
COMPUTER: TENDED COMPATIBLE
COMPUTER: TENDED COMPATIBLE
COURTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
FILING DATE: 06-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                               APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFICATION: 435
PURCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/681,702
FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
RESPERENCE/DOCKET NUMBER: 00786/071002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFRAX: 200154
COMPUTER: IBM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.6
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-07-864-475A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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US-08-468-249A-7
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Gaps

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Sequence 17, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Rosen, Graig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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CORRESPONDENCE ADDRESS: A
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/202,986
FILING DATE: February 25, 1994
ATTORNEY-AGEWT INFORMATION:
NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REGISTRATION NUMBER: 34235
REGISTRATION NUMBER: 34235
REGISTRATION NUMBER: 44168-DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION DATA
TELECOMMUNICATION DA
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100.0%; Pred. No. 0.00081;
ive 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 amino acids
TYPE: amino acid
STRANDEDNESS: single
                        130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.4
Best Local Similarity 100.
Matches 13; Conservative
                                                                                      Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 LHCTRNYIHMHLF 184
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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ZIP: 07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6 Becarding:
                                                    Boston
                                                                                                                                          02109
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                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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APPLICANT: HOSOYA, Masaki
APPLICANT: HOSOYA, Masaki
APPLICANT: HOSOYA, Masaki
APPLICANT: MIXAMOTO, Yasunori
APPLICANT: HIXAMOTO, Yasunori
APPLICANT: HABATA, Yugo
APPLICANT: SHIMAMOTO, No. 585878710
APPLICANT: SHIMAMOTO, No. 580878710
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                   Sequence 2, Application US/08112817C
Patent No. 5573928
GENERAL INFORMATION:
APPLICANT: Hsiung, Hansen M.
APPLICANT: Smith, Dennis P.
APPLICANT: Shang, Xing-Yue
TITLE OF INVENTION: RCCEPTOR
INUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh IIci compatible
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word for Macintosh v.5.la
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,817C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13; DB 1; L
Pred. No. 0.00031;
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                                                                                                                                                                                                                                                                                                                STREET: Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Application US/08811897A Patent No. 5858787 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATJORNEY/AGENT INFORMATION:
NAME: MULPHy, Richard B.
REGISTRATION NUMBER: 35,296
REFERENCE/DOCKET NUMBER: x-92;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3589
TELEPHONE: 317-276-3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.4%; Sox
Best Local Similarity 100.0%; P.
Matches 13; Conservative 0;
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INFORMATION FOR SEQ ID NO: 2:
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OHTAKI, Tetsuya
MASUDA, Yasushi
KITADA, Chieko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-112-817C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 LHCTRNYIHMHLF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 LHCTRNXIHMHLF 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-811-897A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                     RESULT 24
US-08-112-817C-2
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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100.0%; Pred. No. 0.084;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FELOPY disk
COMPUTER FELOPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,631
FILING DATE: July 1, 1993
CLASSIFICATION 1435
PRIOR APPLICATION DAMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATFORNEY/AGENT INFORMATION:
NAME: MCMASTERS, DAUG-1992
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION INFORMATION:
TELEPRAK: 206-622-4900
THEORYMINICATION INFORMATION:
TELEPRAK: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08452930
Patent No. 5919635
GENERAL INFORMATION:
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICAMT: Kindsvogel, Waylne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
                                                                                                                                                ; Sequence 18, Application US/08086631
; Patent No. 5776725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
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LENGTH: 162 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 99104-7092
COMPUTER READABLE FORM:
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                           99 LVEGLYLHNL 108
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ZIP: 99104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEATTLE
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                                                                                                        RESULT 28
US-08-086-631-18
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US-08-452-930-18
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STATE:
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                                                                                                                                                                                                                                                                                                              1.8%; Score 10; DB 3; Length 10;
100.0%; Pred. No. 0.007;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
COUNTRY: USA
ZIP: 99104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,956
FILING DATE: 30-MAY-1995
'TASSTFICATION: 530
              33,073
ner: 325800-458 (PF201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kindsvogel, Waylne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 18, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
NAME: MULLINS, J.G.
REGIESTRATION NUMBER: 33,073
REFRENCE/CDCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                              Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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MOLECULE TYPE: protein

US-08-453-956-18
                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                               120 ANYSDCLRFL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08845546
Patent No. 6077949
GENERAL INFORMATION:
APPLICANT: Munroe, Donald
APPLICANT: Gupta, Ashwani
APPLICANT: Mcallum, Kirk
APPLICANT: Fan, Ermei
TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
TITLE OF INVENTION: 2 RECEPTORS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match . 1.8%; Score 10; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.11;
                                                                              990008.424C1
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FILING DATE: 24 APR-1997
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Friebel, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8607-018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 100000
TELECAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
                                       REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 99000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                   McMasters, David D.
                                                                                                                                                                                                                                                           : 162 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein PCT-US93-08174-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 LVEGLYLHNL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 LVEGLYLHNL 264
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                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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Pred. No. 0.084;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURBINT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08174

TITING DATE: 30-AUG-1993
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA: US/08/452,930
FILING DATE: US-MAY-1995
CLASSIFICATION NUMBER: US/08/6531
FILING DATE: JOHN 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: JOHN 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAME: ZymoGynetics, Inc.
APPLICANT: STREET: 4225 Roosevelt Way North East
APPLICANT: CITY: Scattle, Washington
APPLICANT: CUNTRY: United States
APPLICANT: POSTAL CODE: 98105
APPLICANT: TELEPHONE: (206) 547-80808
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
PCT-US93-08174-18
; Sequence 18, Application PC/TUS9308174
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 10; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-452-930-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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APPLICANT:
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1.8%; Score 10; DB 1; Length 477;
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ZIP: 99104-7092

COMPUTER READBLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,930
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                      APPLICATION NUMBER: US/08/086,631
FILING DATE: July 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTONEY/AGENT INFORMATION:
NAME: MCMAS.TETS, DAVID D.
REGISTRATION NUMBER: 990008.424C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.2 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/08452930
Fatent No. 5919635
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: SEATLE
CITY: SEATLE
STATE:
WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/ACENT INFORMATION:
NAME: MCMASLERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 206-682-6031 INFORMATION FOR SEQ ID NO: 25:
                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-086-631-25
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111111111
243 LVEGLYLHNL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 LVEGLYLHNL 264
                      COUNTRY: USA
ZIP: 99104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-08-452-930-25
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA

ZIP: 99104-7092

ZIP: 99104-7092

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,956
FILING DATE: 30-MAY-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTOMENY-AGENT INFORMATION:
MANE: AUG-1992
ATTOMENY-AGENT INFORMATION:
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Patent No. 5776725
GENERAL INFORMATION:
TITLE OF INVENTION: GLUCAGON RECEPTORS;
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
Mismatches
                                                                                                                                                                                      Sequence 25, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: GLUCAGON RECEPTORS
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: SEED AND BERRY
CHARLES OF SEQUENCES:
    ADDRESSEE: SEED AND BERRY
CHARLES OF SECUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELECOMMUTCATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
                                                                                                                                                                                                                                                                                                                   STREET: SEATLE STATE: STATE: WA
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0
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INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 477 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-453-956-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 LVEGLYLHNL 264
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243 LVEGLYLHNL 252
                                           172 LHCTRNYIHM 181
                                                                  20 LHCTRNYIHM 29
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Pred. No. 0.23;
         Indels
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                                                                                                                                                                                                                                                                                          APPLICANT: Fan, Ermei
TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
TITLE OF INVENTION: 2 RECEPTORS
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       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Friebel, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8607-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08845546
Patent No. 6077949
GENERAL INFORMATION:
APPLICANT: Munroe, Donald
APPLICANT: Gupta, Ashwani
APPLICANT: McCallum, Kirk
APPLICANT: Fan, Ermel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/AMF
                                                                                                                                                                Sequence 2, Application US/08845546
Patent No. 6077949
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                   APPLICANT: Munroe, Donald APPLICANT: Gupta, Ashwani APPLICANT: Vyas, Tejal APPLICANT: McCallum, Kirk APPLICANT: Fan, Ermei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-790-9090
TELERAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
     Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CON OPERATING SYSTEM:
                                                            243 LVEGLYLHNL 252
                                         255 LVEGLYLHNL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 LHCTRNYIHM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 LHCTRNXIHM 174
                                                                                                                                                                                                                                                                                                                                                                                                                          New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                RESULT 36
US-08-845-546-2
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STATE:
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0
                                                                                                                                                                                                                   Length 477;
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                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08174
FILING DATE: 30-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                North East
                                                                                                                                                                                                                 1.8%; Score 10; DB 2;
100.0%; Pred. No. 0.22;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990008.424C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAME: ZymoGynetics, Inc.
APPLICANT: STREET: 4225 Roosevelt Way J
APPLICANT: CITY: Seattle, Washington
APPLICANT: COUNTRY: United States
APPLICANT: POSTAL CODE: 98105
APPLICANT: PELEPHONE: (206) 547-98088
TITLE OF INVENTION: GLUCAGON RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-08174-25
; Sequence 25, Application PC/TUS9308174
; Sequence 15, Application;
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED AND BERRY
6300 COLUMBIA CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MOMSters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                     TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 amino acids
                                                                                                                                                                                                                 Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206-682-6031
                                                                                                                        ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-452-930-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GLANDMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                          255 LVEGLYLHNL 264
                                                                                                                                                                                                                                                                                                                 243 LVEGLYLHNL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-08174-25
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TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
TITLE OF INVENTION: 2 RECEPTORS
NUMBER OF SEQUENCES: 2
COMPESSED: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CUTT: 1036-27-1038.
COUNTRY: 10.5.A.
ZIPP: 1036-27-1038.
COUNTRY: 10.5.A.
ZIPP: 1036-27-1038.
COUNTRY: 10.5.A.
ZIPP: 1036-27-1038.
CONMUTER: New YORK
NEDIUM TYPE: 1046-27-1038.
CONMUTER: 124-ARE-1097
CURRENT APLICATION DATA: 124-ARE-1097
ATTOREX AGENT TOWN NUMBER: 24-ARE-1097
ATTOREX ATTOREX AGENT WORMATION: 43-
ATTOREX ATTOREX AGENT WORMATION: 12-790-900
TELECHANCE 122-790-900
TELECHANCE 212-869-864
TELECHANCE 213-869-864
TELECHANCE 213-869-864
TELECHANCE 213-869-864
TOOLOGY: WALCH 131-81
TOPOLOGY: WALCH 132-860
TOPO
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